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June 18, 2004, 19:17:05; Search time 60 Seconds (without alignments) 1290.300 Million cell updates/sec
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1496
1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                      1586107 seqs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: __geneseqp1980s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	4	Description		1617		Abg26726 Novel hum			Aap70155 Sequence	Aap70590 Sequence	Aau32882 Novel hum		ო				Н	Ade64175 Human Pro		G			Aau79454 HLA-G rec	co.	3 HLA-Bw	7 Human	Ade40254 Human NOV
SUMMARIES	;	ar .	AAG64618	AAG64617	ABB50296	ABG26726	AAB43986	AAP80911	AAP70155	AAP70590	AAU32882	AAR12465	AAY07033	AA013073	AA006772	AAR03142	ADE64171	ADE64175	AAR03144	AAR12466	AAU32883	AAR12464	AAU79454	ADD46572	AAR12463	ABP70087	ADE40254
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215 4 AAG64619 369 4 AAM24017 3164 5 AAV26018 3165 3 AAV56208 3165 3 AAV56202 3165 4 AAB5687 310 4 AAU10225 310 2 AAW68912 310 6 AAW68912 310 7 AAW68912	Aag64619 Human can Aam24017 Human BST Abp70088 Human NOV Aay68268 Human leu Aay5222 HLA-A2/A2 Aab58683 HLA-A2/A2 Aab36874 MHC class Aau10225 Human leu Abu08672 Human leu Aaw68385 Chimeric Aau10224 Human par Abu08671 Human par Abu08671 Human par Aay68273 Human par Aay68274 Human leu Aay68274 Human leu	
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ALIGNMENTS

RESULT 1	∞
4	AAG64618 standard; protein; 274 AA.
3	AAG64618;
1,	12-SEP-2001 (first entry)
Ħ	Human cancer cell specific HLA-F antigen SEQ ID 5.
H	HLA-F antigen; cancer cell specific; human.
Ħ	Homo gapiens.
is Na:	JP2001095584-A.
7 20:	10-APR-2001.
ig K	30-SEP-1999; 99JP-00279566.
	30-SEP-1999; 99JP-00279566.
PA PA	EGAW/) EGAWA K. (MEDI-) MEDINET KK. (KIMU/) KIMURA K.
	WPI; 2001-360493/38. N-PSDB; AAH45556.
	Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
	Claim 2; Page 10-11; 12pp; Japanese.
F - F - F - F - F - F - F - F - F - F -	This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the
	antigen. The antiger
	in which the protein 18 used
i in	etect anti-HLA-F antibodies in bodily illids of the patient. The present
	i)
	Sequence 274 AA;
Query Market Loc	Query Match 100.0%; Score 1496; DB 4; Length 274; Best Local Similarity 100.0%; Pred. No. 1.3e-133; Arabida 0: Gaps
בום ר	
δŸ	1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60

This invention relates to a cancer cell specific HIA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HIA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HIA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HIA-F antigen of the 120 120 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGGCLELLRRYLENGKETLQ 180 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180 240 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGBEQTQDTBLVBTRPAGDGT 240 Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer. EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT Human cancer cell specific HLA-F antigen SEQ ID FORWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274 HLA-F antigen; cancer cell specific; human. Disclosure; Page 9-10; 12pp; Japanese. AAG64617 standard; protein; 362 99JP-00279566. 99JP-00279566 (first entry) 2001-360493/38. EGAWA K. MEDINET KK. (MEDI-) MEDINET KE (KIMU/) KIMURA K. WPI; 2001-360493/ N-PSDB; AAH45555 Sequence 362 AA; JP2001095584-A. 30-SEP-1999; Homo sapiens 30-SEP-1999; 12-SEP-2001 10-APR-2001. invention 121 121 181 61 61 181 241 (EGAW/) 음 ò Ωp ò 6 원 ò Dp ò

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; crystadenofibroma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; padenofibroma; adenofibroma; pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; HLA-Cw ovarian tumour marker protein, SEQ ID NO:82. Hough CD; Sherman-Baust CA, Pizer ES, (USSH) US DEPT HEALTH & HUMAN SERVICES ABB50296 standard; protein; 362 AA 03-APR-2001; 2001WO-US010947. 03-APR-2000; 2000US-0194336P. (first entry) gene therapy; vaccine WO200175177-A2. sapiens. 11-OCT-2001. 08-FEB-2002 Morin PJ, ABB50296; HOMO ABB50296

82 EWTTGYAKANAQTDRVALRNLIRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141

RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT

142 181

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KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLO

202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEOTODTELVETRPAGDGT

FORWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274 262 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295

241

Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker

WPI; 2001-626450/72. N-PSDB; ABA83122.

23; Page 126-127; 140pp; English Claim The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA831081-ABA83122, ABA83180, ABA831812 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA831819). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer, in tests for monitoring disease status in a patient behing treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (1.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenoma,

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Length 362; Indels 9

EWTTGYAKANAQTDRVALRNLLRRYNQSBAGSHTLQGNNGCDMGPDGRLLRGYHQHAYDG 120

61

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22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81

1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTOFLRFDSDAAIPRMEPREPWVEQEGPQYW

100.0%; Score 1496; DB 4; 100.0%; Pred. No. 1.9e-133; ive 0; Mismatches 0;

274; Conservative

Best Local Similarity Matches 274; Conserv

Query Match

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mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membranelocalised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded prevention of ovarian cancer. Sequences ABBSO257-ABBSO299 represent proteins encoded by ovarian tumour marker genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
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imaging, diagnostic, genetic disorder.
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23-AUG-2000; 2000US-00649167
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food supplement; medical in
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N-PSDB; AAS90913.
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                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                 Sequence 362 AA;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, ollogomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed control in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (II) are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 677;
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Pred. No. 1.3e-132;
0; Mismatches 1; Indels
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                                                                                                                 English.
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                                                                                                                 57085; 103pp;
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27-JAN-1988;
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18-SEP-1990
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                                                                                                                                                                                                                                                                                                                                 AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antidiathritic; antidiathritic; antidiametory; antithyroid; antialerator, antibaterary; immunomodulator; coagulant; or notropic; vasotropic; antipsoriatic and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoistic cells, autoimmune closed to treat immune disorders by activating or inflammation, modulate haemostatic or thrombolytic activity, modulate coaction, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44440 represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                         Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                               Claim 11; Page 2115-2116; 2352pp; English.
                                                                                                                                                          99US-0124270F.
                                                                                                                                 2000WO-US005882
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Best Local Similarity 99.6
Watches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
                                                                                                                                                                                                           Ruben SM;
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FR 269
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                                                                                                                                                        Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide corresp. to major histocompatibility antigen regions - use for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "alpha-1 region"
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AAP80911 standard; protein; 274 AA
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87US-00138547.
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Best Local Similarity 82.8'
Matches 227; Conservative
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                                                                                            (revised)
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205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLIWQRDGEDQTQDTELVETRPAGDRT 264
                                                                                                                                                                                                               Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      - and diagnostic reagents contg. such DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
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                                                                                                                                                                                       Sequence of the human histocompatibility antigen HLA
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82.5%; Pred. No. 5.7e-108;
ive 14; Mismatches 33;
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                         FOKWAAVVVPSGEEQRYTCHVQHEGLPOPLILRW 274
                                       POKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW
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                                                                                                                AAP70590 standard; protein; 337
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Best Local Similarity 82.5
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 337 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded by genomic DNA encoding human histocompatibility antigen
                  THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 matibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)
     RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding for human histocompatibility antigen HLA-B 27
                                                                                                                                                                                                                                                                                Ankylosing spondylitis; rheumatic disorder; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.1%; Score 1228; DB 1;
llarity 82.1%; Pred. No. 5.6e-108;
Conservative 14; Mismatches 35;
                                                     274
                                                               FQXWAAVVVPSGEEQRYTCHVQHBGLPKPLTLRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meo
                                                     FOXWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 6; 13pp; German.
                                                                                                                                          AAP70155 standard; protein; 362
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                                                                                                                                                                                                                                                                                                                                                                                  86EP-00116139.
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85DE-03545576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dorner
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                         (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-171469/25
N-PSDB; AAN70225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weiss E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1985;
21-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 225;
                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1986;
                                                                                                                                                                                         25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                          24-JUN-1987
                                                                                                                                                                                                       10-MAR-1993
03-APR-1991
                                                                                                                                                                                                                                                                                                                                 EP226069-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Szots H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                   AAP70155;
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208 RADPPKTHVTHHPISDHEATLRCWALGFYPABITLIWQRDGEDQTQDTELVETRPAGDRT 267
181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                            268 FQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 301
                                                                     241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-182989/25.
N-PSDB; AAQ12116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 366 AA;
                                                                                                                                                                                                                                                                                                                                HLA-C exon Cb-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP03112485-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1991.
                                                                                                                                                                                                                                                                         25-MAR-2003
29-AUG-1991
                                                                                                                                                                                                                                        AAR12465;
                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                    class
                                                                                                                                                                   RESULT 10
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                                    D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells corpressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the cucles and cells genetically engineered to express them are also useful for producing the proteins. The proteins of a nutritional supplements. They may be used to increase stem cell or proliferation; to regulate haematopoises; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU33810-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRNIQIFKINIQIDESLRNLRGYYNQSEAGSHILQSMYGCDVGPDGRLLRGHNQYAXDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDYISLNEDLRSWTAADTVAQITQRFYBAEEYABEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 GSHSWRYPDTAMSRPGRGEPRISVGYVDDTQPVRFDSDAASPREEPRAPWIEQEGFBYW 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVBQEGPQYW
                                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 1224; DB 4; Length 369;
81.0%; Pred. No. 1.4e-107;
ive 21; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 683; 765pp; English.
                                                           AAU32882 standard; protein; 369 AA.
                                                                                                                                                                   Novel human secreted protein #3373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT;
                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                   WO200179449~A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222;
                                                                                                                                  18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                     25-OCT-2001
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                                                                                            AAU32882;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 RETOKYKROAQTDRVSLRNIRGYYNQSEAGSHTLQWMFGCDLGPDGRLLKGYDQSAYDGK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 SHSWRYFSTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASFRGEPRAÞWVBQBGPBYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 WITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 DYISLNEDLRSWIAADTVAQITQRFYEAEBYABEFRIYLEGECLELLRRYLENGKETLQR
                                                                                                                                                                                                                 leukocyte antigen; probe; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-C gene, DNA probe and transformant cells - for immunisation animals and monoclonal antibody development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.8%; Score 1209; DB 2;
81.7%; Pred. No. 3.7e-106;
iive 18; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 QKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 2; 13pp; Japanese
AAR12465 standard; protein; 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OLYU ) OLYMPUS OPTICAL CO LID
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Best Local Similarity 81.7<sup>3</sup>
Matches 223; Conservative
                                                                                                 (revised)
(first entry)
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265 FOKWAAVVVPSGEEQRYTCHVQHEGLPEPLTLRW 298 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274

241

AA013073 standard; protein; 374 AA

RESULT 12 AAO13073 ID AAO1

181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT

DRETOKYKROAQTDRVSLRNLRGYYNOSEAGSHIIQRMYGCDVGPDGRLLRGYDQYAYDG KDYISLNEDLRSWTAADTVAQITQRPYEABEYABEFRTYLEGECLELLRRYLENGKETLQ

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                                Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stockert E, Gure A, Chen Y, Gout Pfreundschuh M, Tureci O, Sahin U;
                                                                                                                                                                                                  Breast cancer associated antigen precursor sequence.
266 QKWAAVMVPSGEEQRYTCHVQHEGLPEPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 417-418; 787pp; English.
                                                                                                  AAY07033 standard; protein; 366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00896164,
97US-0061599P.
97US-0061765P,
97US-00948705,
97GB-00021697,
                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US014679,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00102322.
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scanlan MJ,
Obata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-132448/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 366 AA;
                                                                                                                                                                                                                                                                    prostate cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                 02-JUL-1999
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                    WO9904265-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-1997;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Old LJ, Sc
O'hare M,
                                                                                                                                 AAY07033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                             Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                         Human polypeptide SEQ ID NO 26965.
                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI93004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 374 AA;
                                                                                                                                                                                                                                                                        WO200164835-A2.
                                                                                                                                                                                                                                   Homo sapiens
                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                07-SEP-2001.
                  AA013073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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61 BWTTGYAKANAQIDRVALRNLLRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120

25 GSHSMRYFYTAVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYW 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW

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80.6%; Score 1206; DB 2; Length 366; 81.0%; Pred. No. 7.1e-106; ive 18; Mismatches 34; Indels

Best Local Similarity 81.0 Matches 222; Conservative

Query Match

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Indels

.5; 1e-105; 34; DB 4;

80.5%; Score 1204.5; 81.8%; Pred. No. 1e-1 .ive 15; Mismatches

Length 374;

120 144 180 204 240

84

264

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1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                       25 GSHSKRYFYTAMSRPGRGEFRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIEQEGPBYW
                                                                                                                                            EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                             KDYISLNEDLRSWTAADTVAQITQRFYEAEEYABEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                           1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                 RADPPKAHVAHHPISDHBATLRCWALGFYPABITLTWQRDGBBQTQDTBLVBTRPAGDGT
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Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomedulatory activity and activity, tissue growth factor activity, immunomedulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                   273
                                                   WITGYAKANAQIDRVALRNILIRRYNQSBAGSHILQGMNGCDMGPDGRLLRGYHQHAYDGK 121
                                                                    RETOKYKRQAQIDRVSLRNLRGYYNQSEAGSHTLQWMYGCDLGFDGRLLRGYDQSAYDGK 153
                                                                                                      181
                                                                                                                              DYIALNEHLRSCTAADTAAQITQRKWEAARAAEQWRAYLEGTCVEWLRRYLENGKETLQR 213
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                          93
  61
                                                                                                                                                                           214 AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTF
                SHSMRYFYTAVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYWD
                                                                                                                                                         ADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTF
  SHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWE
                                                                                                      DYISINEDLRSWIAADTVAQITORFYBAEEYAEEFRIYLEGECLELLRRYLENGKETLOR
                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell proliferation, cell differentiation, gene the vaccine, peptide therapy, stem cell growth factor, haematopolesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorders, arthritis, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                               OKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 20664.
                                                                                                                                                                                                                                                                                                        AAO06772 standard; protein; 374
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI86703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA for class 1 human leucocyte antigens - with derived probes and
transformed cells, used for DNA typing, as immunogens etc.
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80.3%; Pred. No. 2.1e-105;
iive 20; Mismatches 34;
                                               265 POKWAAVVVPSGEEORYTCHVOHEGLPKPLTPERW 299
241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLI-LRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 13; 23pp; English.
                                                                                                                                                                                   AAR03142 standard; protein; 362 AA
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction tinjury (CCI) and spared nerve injury (SINI) in an animal (e.g. spinal therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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The invention discloses a composition comprising two or more isolated ratter human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymuclectide sequence which is differentially expression of a polymuclectide sequence which is differentially compound that regulates the activity of one or more of the polymuclectides, a method for pain, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                240
                                                EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                   KDYISLNEDLRSWIAADTVAQITQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                   84
RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                                   265 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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es 220; Conserva
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Job time : 63 secs
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APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: KRENSKY, ALAN M.
APPLICANT: PARHAM, PETER
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
CITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%; Score 44; DB 1; Length 274 ilarity 100.0%; Pred. No. 1.2e-35; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON
STATE: DC
CUMNIKY: USA
ZIP: Z0006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIDLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN PC-BOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATA:
FILING DATE: 05-APR-1994
CLASSIPICATION: 42-41994
US-08-481-985B-101

US-08-65-23

US-08-314-476-23

US-08-370-476-99

US-08-370-476-99

US-08-370-476-100

US-08-370-476-1100

US-08-370-476-1100

US-08-370-476-1100

US-09-444-05-83

US-08-481-985-83

US-08-481-985-82

US-08-481-985-82

US-08-481-985-82

US-08-481-985-82

US-08-481-985-82

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US-08-481-985-82

US-08-481-985-82

US-08-481-985-80

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US-08-481-985-80

US-08-481-985-80
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NAME: MILMAN, ROBERT A.
REGISTRATION UNDERS: 36,217
REFERENCE/DOCKET UNDERS: 2860-20200.22
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 494-0792
TELERA: 90-4030 MRGNFOGRSWSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                      US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
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amino acid
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TOPOLOGY: linear
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 US-08-222-851-1
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Sequence 8, Appli
Sequence 8, Appli
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 105, Appl
Sequence 107, Appl
Sequence 97, Appl
Sequence 98, Appl
Sequence 98, Appl
                                                                         June 18, 2004, 19:28:42; Search time 22 Seconds (without alignments) 642.978 Million cell updates/sec
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Sequence
Sequence
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1 GSHSLRYFSTAVSRFGRGEP.....QRYTCHVQHEGLPQPLILRW
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.: /cgn2 6/ptodata2/jaa/5B_COMB.pep:*
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.: /cgn2 6/ptodata2/jiaa/PCTUS COMB.pep:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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3-08-484-905-98
3-08-484-905-99
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                                                                                                                                                                                                        389414 segs, 51625971 residues
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                                                                               Run on:
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Gaps

; 0

Length 274;

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Sequence Application US/08406057;
Patent No. 5856442;
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MORRAL, PHILIPPE
APPLICANT: KIRSZENAN, MAREN
APPLICANT: KIRSZENAN, MAREN
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAX, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%; Score 39; DB 3; Length 117; 100.0%; Pred. No. 4.8e-31; tive 0; Mismatches 0; Indels
1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                          COUNTY: USA

ZIP: 2202

COMPUTER READABLE FORM:
MEDITOR TYPE: Tape
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 127-0CT-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR.1994

ATTORNEY/AGENT INFORMATION:
NAME: OBLCN, NORMAN F

RESERVENCE/POCKET NUMBER: 24,618

REFERENCE/POCKET NUMBER: 0846-0437-0

TELECOMMUNICATION NUMBER: 0846-0437-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 39; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                    ARLINGTON
VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-406-057-8
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                                                                                                                           Sequence 9, Application US/08406057
| Sequence 9, Application US/08406057
| GENERAL INPORMATION:
| APPLICANT: CAROSELIA, EDGARDO D
| APPLICANT: MOREAU, PHILIPPE
| APPLICANT: GIUCKMAN, ELLANE
| APPLICANT: KISSENBAUM, MAREK
| TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
| TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
| NUMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
| STREET: 1155 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
| CITY: ARLINGTON
| STATE: VIRGINIA
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08958316
Fatent No. 6291659
GENERAL INFORMATION:
APPLICANT: CAROSELA, EDGARDO D
APPLICANT: GLUCKNAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 39; DB 2; Length 117; 100.0%; Pred. No. 4.8e-31; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER EADABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Warches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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MOLECULE TYPE: peptide
US-08-406-057-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-958-316-9
                                                                            RESULT 2
US-08-406-057-9
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Gaps

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PEREIN NO. 597-5531

PEREIN NO. 597-5531

PERILCANT. MORTEAL, Estelle

PEPLICANT. MORTEAL, SETELLE

PEPLICANT. Abatedo, Jean-Pierre

PEPLICANT. Abatedo, Jean-Pierre

PEPLICANT. COUNTISTY, Philippe

TITLE OF INVENTION. Complex(MFC) Determinant and Methods for Using the TITLE OF INVENTION. Determinant

NUMBER OF INVENTION. Determinant

NUMBER OF SEQUENCES: 127

OCRESSORES Durner

STREET: 1300 I Street, N.W., Suite 700

STATE: D.C.

STREET: 1300 I Street, N.W., Suite 700

STATE: D.C.

STREET: 1300 I Street, N.W., Suite 700

STATE: D.C.

SOFTWARE: D.C.

COMPUTER READABLE FORM.

MEDIUM TYPE: PLORPY DISK

COMPUTER READABLE FORM.

MEDIUM TYPE: 1800 FOCS-MS-DOS

OFFRANTIG SPERM: PC-DOS-MS-DOS

OFFRANTIG SPERM: DOS-MS-DOS-MS-DOS

OFFRANTIG SPERM: PC-DOS-MS-DOS

OFFRANTIG SPERM: DOS-MS-DOS-MS-DOS

OFFRANTIG SPERM: DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-MS-DOS-M
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10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                         Length 145;
                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                 79 ELVETRPAGDGTFQKWAAVVVPSGBEDRYTCHVQHEGLP 117
                                                                                                                                                                                                                                            229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
                                                                                     Score 39; DB 3; LA
Pred. No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 QDTELVETRPAGDGTFOKWAAVVVPSGEEQ 255
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                                                                                     Query Match 14.2%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 5.9 Matches 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 289 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-481-985B-79
            US-08-958-316-8
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CORRESPONDENCE ADDRESS:
ADDRESSER: OBLOW, SPLYARK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2002
ZIP: 2003
ZIP: 2003
ZIP: 2003
ZIP: 2003
ZIP: 2004
ZIP: 2005
ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08958316
Patent No. 6291659
GENERAL INFORMATION:
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKAN, ELLANE
APPLICANT: GLUCKAN, ELLANE
APPLICANT: TRANSCRIPS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ELVETRPAGDGTFÇKWAAVVVPSGBEQRYTCHVQHBGLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

14.2%; Score 39; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 39; Conservative 0; Mismatches 0;
FILING DATE: 18-MAR-1994

JATORNEY AGENT INFORMATION:

NAME: OBLON, NORMAN E.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 846-331-0

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELERAX: (703) 413-3200

TELERAX: (703) 413-3200

TELERAX: (703) 413-220

TELERAX: 148855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 145 amino acids

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

NOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-958-316-8
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US-484-905-105

US-484-905-105

Sequence 105, Application US/08484905

Patent No. 597651

GENERAL INFORMATION:

APPLICANT: Mosteac, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Acurilsky, Philippe
TITLE OF INVENTION: Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBERS OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
STREET: 10005-315

COMPUTER READABLE FORM:
MEDIUM TYPE: RIADABLE FORM:
MEDIUM TYPE: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
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                                                               STREEL: 15005.

CITY: Machington
STATE: D.C.
ZIP: 20005.
ZIP: 20005.
ZIP: 20005.
ZIP: 20005.
ZIP: 20005.
ZIP: Ploppy disk
COMPUTER: EALDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION NUMBER: US 08/117,575
PRIOR APPLICATION NUMBER: US 08/117,575
FILING DATE: 06-JUN-1993
PRIOR APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 05-146
REPREMENCE/DOCKET NUMBER: 05-146
REGISTRATION NUMBER: 05-146
REGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.9%; Score 30; DB 3; Le.
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 ODTELVETRPAGDGTFOKWAAVVVPSGEEQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 ODTELVETRPAGDGTFOKWAÁVVVPSGEEQ 255
    ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-370-476-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
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GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
APPLICANT: Colous, David
APPLICANT: Ojcius, David
APPLICANT: Ojcius, David
APPLICANT: Orive, Yaranda
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Sequence 79, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abustado, Jean-Pierre
APPLICANT: Mourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 289; 9.4e-22;
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ADDRESSE:
ADDRESSE:
DULING
CITY:
Washington
STATE:
D.C.
ZTATE:
D.C.

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10.9%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 9.4
Matches 30; Conservative 0; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
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MOLECULE TYPE: peptide

US-08-481-985B-79
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US-08-370-476-79
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224 OTODIELVETRPAGDGTFOKWAAVVVPSG 252
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TELEPHONE: 202-100

TELEPAX: 202-400

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

"VPE: amino acid

1'inear
                                                                                                                                                                                              LENGTH: 274 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-107
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-108
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Facquence 107, Application US/08484905

Patent No. 5976531

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Rourilsky, Philippe

TITLE OF INVENTION: Complex(MFC) Determinant and Methods for Using the

TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSE: Pinnegan, Henderson, Farabow, Garrett &

ADDRESSE: Dunner

STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 29; DB 2; Length 274; 100.0%; Pred. No. 8.8e-21; tive 0; Mismatches 0; Indels
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CITY: Washington
CITY: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FLING DATE: 07-JUNE-1995
CLASSIPICATION 330
PRIOR APPLICATION: 530
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIPICATION: DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/484,905
FILING DATE: US-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
ATTORNEY-AGENT INFORMATION:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY-AGENT INFORMATION:
NAME: POETER, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 OTODIELVETRPAGDGIFOKWAAVVVPSG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-105
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Best Local Similarity
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US-08-484-905-107
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RESULT 11

REPREMAL INFORMATION

RESULT 11

APPLICANT: Routining Malex Histocompatibility

ITILE OF INVENTION: Complex (MHC) Determinant and Methods for Using the TITILE OF INVENTION: Complex (MHC) Determinant and Methods for Using the TITILE OF INVENTION: Determinant

RUMBER OF SCOURNES: 127

RUMBER OF SCOURNES: 127

CORRESSES: Pinnegan, Henderson, Farabow, Garrett & ADRESSES: Dunner

STREET: 100

GITY: Meshington Street, N.W., Suite 700

GITY: Meshington 1 Street, N.W., Suite 700

GITY: Meshington 1 Street, N.W., Suite 700

STREET: 2006-318

REDIUM TYPE: Flopy Disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy Disk

COMPUTER: 18P C compatible

OFFRAING STEME: D-C.

STREET: 3006-318

REDIUM TYPE: Flopy Disk

COMPUTER: 18P C compatible

OFFRAING STEME: D-C.

STREET: 3007-318

REPREMATION DATE: 307-418-1995

FILING DATE: 05-DEC-1991

CLASSIFICATION DATE: 33.32

RIGHER APPLICATION DATE: 33.32

RIGHER POLICY: Jane B. R.

RESISTRATION NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

NAME: POLICY: Jane B. R.

RESISTRATION NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

REPREMED: POLICY: Jane B. R.

RESISTRATION NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

REPREMED: POLICY: Jane B. R.

RESISTRATION NUMBER: 03495.0106-03000
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                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%; Score 29; DB 2; Le
100.0%; Pred. No. 8.8e-21;
:ive 0; Mismatches 0;
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-400-4000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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, MOLECULE TYPE: peptide US-08-481-985B-107
GENERAL INFORMATION
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                                                                              Gaps
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0
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APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Dan-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                        10.6%; Score 29; DB 2; Length 274; 100.0%; Pred. No. 8.8e-21; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
ZIP: 20005-3315
COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION 1435
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: 235,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INPORMATION:
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                                                                                                                              224 QTQDTELVETRPAGDGTFQKWAAVVVPSG 252
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; Patent No. 6011146
                                                                                                                                                                                                                                                   RESULT 12
US-08-481-985B-105
US-08-481-985B-105
Sequence 105, Application US/08481985B
Secuence 105, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Notice:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCH: 274 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 29; Conservative
                                                                              Conservative
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MOLECULE TYPE: peptide
US-08-481-985B-105
                           Query Match
Best Local Similarity
Matches 29; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-481-985B-107
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APPLICANT: Mostea Catalier

APPLICANT: Abseracio, Jean-Pierre
APPLICANT: Abseracio, Jean-Pierre
APPLICANT: Abseracio, Jean-Pierre
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: Altered Major Histocompatibility Complex
CORRESSER: Pinnegan, Henderson, Parabow, Garrett &
ADDRESSER: Dunneg S. 148

CORRESPONDENCE PINNESS:
ADDRESSER: Dunnegan, Henderson, Parabow, Garrett &
ADDRESSER: Dunnegan, Henderson, Parabow, Garrett &
ADDRESSER: Dunnegan, Henderson, Parabow, Garrett &
CORRESPONDENCE PINNESS:
CORPTER TOWN COMMANDERS: USON COMMANDERS OF COMMANDERS OF COMMANDERS: USON COMMANDERS: UNIVERSITY AND COMMANDERS: UNIVERSE OF UNIVERSITY AND COMMAND COMMAN
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Search completed: June 18, 2004, 19:32:29 Job time : 23 secs
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Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-370-476-105
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Sequence 105, 409

Sequence 105, 409

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Kourilsky, Philipe

APPLICANT: Kourilsky, Philipe

APPLICANT: Casrouge, Armanda

TITLE OF INVENTION: Altered Major Histocompatibility Complex

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.6%; Score 29; DB 3; Length 274; Best Local Similarity 100.0%; Pred. No. 8.8e-21; Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREY APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/801,818
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLESSIFICATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4000
SEGURATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-481-985B-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-370-476-105
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FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION NUMBER: US 07/792,473
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mayers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,46
REGISTRATION NUMBER: 25,000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acide
TYPE: mino acide
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1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274
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2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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		12-851-1  22-851-1  20-851-1  ADDIICATION IN TENENGRATION: FUICANT: TENENGRY, ALEPLICANT: PARHAM, PET FUICANT: PARHAM, PET FUICANT: PARHAM, PET FUICANT: PARHAM, PET FUIE OF INVENTION: FUEE OF INVENTION: AC FUEE OF INVENTION FUEE STATE: DC COUNTY: MASHINGTON FUEE TO TOOM FUEL TO TOOM FUE	'vat	STAY  :  rTST
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181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTBLVBTRPAGDGT 240
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                                                                                                                            85 DGETRKVKAHSQTHRVDLSTLRGYYNQSEAGSHIVQRMFGCDVGSDGRFLRGYHQYAYDG 144
GSHSLRYPSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRWEPREPWVEQEGPQYW
                           25 GSHSKRYFYTSVSRPGRGEPRFIAVGYVDDTOFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                                                                                                                              121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                                                   Sequence 100 Application US/08481985B
; Sequence 100 Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
APPLICANT: Motated Stelle
APPLICANT: Motated, Jean-Pierre
APPLICANT: Motated, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
ADDRESSE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STRIE: D.C.
ZIP: 20005-1315
COMPUTER READABLE FORM:
MEDIUM TYPE: Flormy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.1%; Score 1154; DB 3; Length 365; 76.6%; Pred. No. 1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: OF-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                              265 POKWAAVVVPSGQEORYTCHVOHEGLPRPLTLPW 298
                                                                                                                                                                                                                                                                                                                                                                                        241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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US-08-481-985B-100
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                                                               KDYISINEDIRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLEILRRYLENGKETLQ 180
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                                                                                                                                                                                                                               181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mottez, Estelle
APPLICANT: Mosteado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(WHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF INVENTION: Determinant
CORRESPONDENCE: 127
CORRESPONDENCE ADDRESS:
                                   EWITGYAKANAQTDRVALRNLLRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
STRIET: Mashington
STATE: D.C.
ZIP: 20005-1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
1e-104;
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                              241 FOKWAAVVVPSGEBORYTCHVQHEGLPKPLTLRW 274
                                                                                                                                                                                                                                                                                                                        FOKWAAVVVPSGEEQRYTCHVQHEGLPOPLILRW 274
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CIASTPICATION: 530
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: POTTET INFORMATION:
NAME: POTTET 133,332
REGISTRATION NUMBER: 33,332
REGISTRATION NUMBER: 33,332
REGISTRATION NUMBER: 03495.0106-TELEPHONE: 202-498-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 76.6
Matches 210; Conservative
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                                                                                                                                                                                                          KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                   181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                    25 GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGEFYW
                                         1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
  Gaps
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Class I (MHC) protein"
  42; Indels
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Fatent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Grank, Andreas
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: P-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLIG DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                    265 FQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPW 298
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APPLICATION. ..
FILING DATE: 23-rx.
FILING DATE: 23-rx.
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERBOCE/COCKET WINBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGURM: 365 amino acids
TYPE: amino acid
TYPE: amino acid
22; Mismatches
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
NAME/KEY: Protein
;
LOCATION: 1..365
;
OTHER INFORMATION: 0.
US-08-652-265-23
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US-08-652-265-23
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                                                                                                                                                                                    61 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                 25 GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW 84
                                                                                            1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
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                                                Gaps
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APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES:
ADDRESSE: Pennie & Edmonds TT
    Length 365;
77.1%; Score 1154; DB 3; Length 3 77.0%; Pred. No. 1e-104; tive 21; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2811
ZIP: 10036-2811
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
off:NG DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 POKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
PRIOR APPLICATION NUMBER: US 08/630,912
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                          al Similarity 77.03
211; Conservative
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: New York
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    Query Match
Best Local S:
Matches 211,
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APPLICATION NUMBER:
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| Patent No. 6153408
| GENERAL INFORMATION
| GENERAL INFORMATION
| APPLICANT: Abastado, Jean-Pierre
| APPLICANT: Koutilsky, Phillipe
| APPLICANT: Cone. Yu-Cune, Yu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Human Major Histocompatability
Class I (MHC) protein"
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FLING DATE:
FLING DATE:
FLING DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRW 298
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TELEPHONE: 650-493-4935

TELERA: 661-493-5556

TELERA: 66141 PENNIE

TELERA: 66141 PENNIE

SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDENESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
COATION: 1..365

OTHER INFORMATION: Class I ()
US-08-834-497A-23
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US-08-370-476-100
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121 KDYISINEDIRSWTAADTVAQITQRFYEAEBYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.1%; Score 1154; DB 3; Length 365; Best Local Similarity 76.6%; Pred. No. 1e-104; Matches 210; Conservative 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-05-503-444A-23
US-05-503-444A-23
US-05-503-444A-23
Sequence 23, Application US/09503444A
Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
STRFFT.
PELLING DATE: 07-52P-1993

PILLING DATE: 07-52P-1993

PRIOR APPLICATION NUMBER: US 08/072,787

FILING DATE: 06-JUN-1993

PRIOR APPLICATION DATA: US 07/801,818

FILING DATE: US 07/801,818

FILING DATE: US 07/801,818

PRIOR APPLICATION DATA: US 07/792,473

PRIOR APPLICATION NUMBER: US 07/792,473

ATTORNEY/AGENT INFORMATION:

NAME: MAYER: Xenneth J. REGISTRATION NUMBER: 25,146

REGISTRATION NUMBER: 25,146

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 26,243.0001-01000

TELEPHONE: 202-408-4000

INPORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:

LENGTH: 265 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 FOKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 365 amino acids; TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide US-08-370-476-100
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APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Usan-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Mourilaky, Philippe
TITLE ON INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
TITLE OF INVENTION: Determinant
NUMBER OF SEGUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STREET: 0.C.
STREET: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRPDSDAASQRMEPRAPWIEQEGPEYW
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                                                                                                                                                                                                                                                                                                                                  Length 341;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07.-UNE-1995
CLASSIFICATION TOTA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07.-UNME-1995
CLASSIFICATION TANGER: US 07/801,818
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
     ; FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.; CURRENT APPLICATION NUMBER: US/08/890,719A; CURRENT FILING DATE: 1997-07-09; EARLIER APPLICATION NUMBER: 60/021,665; MUMBER OF SEQ ID NOS: 39; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 38  LENTH: 341; TYPE: PATENTH: 340; CENTH: 341; TYPE: PATENTH: 380; ORGANISM: Homo sapiens US-08-890-719-38
                                                                                                                                                                                                                                                                                                                                  77.1%; Score 1153; DB 3; 176.6%; Pred. No. 1.1e-104; ive 22; Mismatches 42;
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FILING DATE: 15-NOV-1991
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
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Best Local Similarity 76.6
Matches 210; Conservative
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Sequence 38, Application US/08890719A
Patent NO. 6075125
GENERAL INFORMATION:
APPLICANT: Bacon, Larry D
APPLICANT: Hunt, Henry D
APPLICANT: Hunt, Henry D
APPLICANT: Fulton, Janet
ITILE OF INVENTION: Production of Antisera Specific to Major
TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.1%; Score 1154; DB 3; 77.0%; Pred. No. 1e-104; tive 21; Mismatches 42;
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                                                                                                                                                                          PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16-May-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 16-May-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 04-May-1996
ATTORNEY AGENT INFORMATION:
NAME: POISBART INFORMATION:
REGISTRATION NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPRAN: 212-90-9090
TELEPRONE: 212-90-9090
TELEPRONE: 212-90-9090
TELEPRONE: 212-90-9090
TELEPRONE: 212-869-9741
INFORMATION FOR SEQ ID NO: 23:
SEGUENCE CHARACTERISTICS:
LENGTH: 365 aming acids
                                                                                                   UMBER: US/09/503,444A
14-Feb-2000
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 365 amino acids
amino acid
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Best Local Similarity 77.08
Matches 211; Conservative
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MOLECULE TYPE: protein
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OTHER INFORMATION:
OTHER INFORMATION:
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US-08-890-719-38
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Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mostes, Estelle
APPLICANT: Mostes, Jean-Pierre
APPLICANT: Mostes, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(FMC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                    76.9%; Score 1151; DB 2; Length 365; 76.3%; Pred. No. 2e-104; ive 23; Mismatches 42; Indels (
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FILING DATE: US/08/484,905
FILING DATE: 07-UNB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: US 07/801,818
FILING DATE: 05-DEC 1991
CLASSIFICATION: 530
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COMPUTER READABLE FORM: MEDIUM TYPE: FLORDYD DISK COMPUTER: 1BM PC COMPUTER: 1BM PC COMPUTER: 1BM PC COMPUTER: 1BM PC COMPUTER: 1BM STSTEM: PC-DOS-/MS-DOS
                                                                                                                                        INFORMATION FOR SEQ 1D NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 365 amino acide TYPE: manno acid TOPOLOGY: linear MOLECULE TYPE: peptide
                                                          33,332
                                                                             REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
               ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,
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Matches 209; Conservative
CLASSIFICATION:
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US-08-484-905-99
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Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVERTION: Altered Major Histocompatibility Complex
TITLE OF INVERTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 22; Mismatches 43; Indels
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STRET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
                                         FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: POCLEST, Jane B. R.
REGISTRATION NUMBER: 33,332
REPRENCE/DOCKET NUMBER: 03499;
TELEPOMINICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide US-08-484-905-104
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-9858-104
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Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     ; Score 1151; DB 3; Length 3; Pred. No. 2e-104; 23; Mismatches 42; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
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           CLASSIPTOATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MAYERS Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495
TELECOMMUNICATION INFORMATION:
TELEFONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acids
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05-DEC-1991
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Best Local Similarity 76.3
Matches 209; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-481-985B-99
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US-08-481-985B-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Abstrado, Jean-Pierre
APPLICANT: Abstrado, Jean-Pierre
APPLICANT: Constilaky, Phillipe
APPLICANT: Constilaky, Phillipe
APPLICANT: Constilaky, Phillipe
APPLICANT: Casrouge, Armanda
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: Altered Major Histocompatibility Complex
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%; Score 1151; DB 3; Length 365; 76.3%; Pred. No. 2e-104; ive 22; Mismatches 43; Indels
                                                                                                                                                      FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECHONE: 202-408-400
TELECHONE: 202-408-400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"TYPE: Floppy disk
"TYPE: Floppy Disk
"TYPE: Floppy Disk
"TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/08370476 Patent No. 6153408
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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Best Local Similarity 76.3
Matches 209; Conservative
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1300 I Street, N.W., Suite 700

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Sequence No. 05.53408

GENERAL INFORMATION:
APPLICANT: Motect, Estelle
APPLICANT: Absatado, Jean-Pierre
APPLICANT: Lone, Yu-Chun
APPLICANT: Lone, Yu-Chun
APPLICANT: Carcuge, Armanda
ITILE OF INVENTION: Altered Major Histocompatibility Complex
ITILE OF INVENTION: Altered Major Histocompatibility Complex
ITILE OF INVENTION: Altered Major Histocompatibility Complex
CARREPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
76.9%; Score 1151; DB 3; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels (
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                 TILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117,575

FILING DATE: 06-70N-1993

APPLICATION NUMBER: US 08/072,787

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

PRIOR APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

APPLICATION NUMBER: 25,146

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05243.0001-
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05243.0001-
TELECOMMUNICATION INFORMATION:

TELEPENCE DOCKET NUMBER: 05243.0001-

TELEPENCE DOCKET NUMBER: 05243.0001-
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-4400
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-370-476-99
                                                                                                  FILING DATE
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61 EWTIGYAKANAQIDRVALRNILLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
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| Patent No. 5976551
| GENERAL INFORMATION:
| APPLICANT: Mottez, Estelle
| APPLICANT: Abastado, Jean-Pierre
| APPLICAN
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARS: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPRAN: 202-408-4000
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 06-UN-1993
PRIOR APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-UN-1993
PRIOR APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NO-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAYERS, KENDERH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 365 amino acids
amino acid
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Washington
                                                                                                       20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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Search completed: June 18, 2004, 19:28:39 Job time : 23 secs

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Sequence 5, Appli
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Sequence 4, Appli
Sequence 1431, Appli
Sequence 7, Appli
Sequence 70, Appli
Sequence 80, Appli
Sequence 80, Appli
Sequence 23, Appli
Sequence 6, Appli
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1496
1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274
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(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*)

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(cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*)

(cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*)

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(cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-257-021-82
0 US-10-408-765A-1887
2 US-09-919-371-4
US-09-925-301-1431
2 US-10-380-880-7
2 US-10-10-172-160
5 US-10-03-463-78
2 US-09-819-371-6
5 US-10-03-463-80
4 US-10-03-463-80
6 US-10-03-888-23
6 US-10-073-300-5
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6 US-10-075-257-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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2017 2017 2017 2017 2017 2017 2017 2017	Sequence 26, Appl Sequence 31, Appl Sequence 34, Appl Sequence 36, Appl Sequence 247, App Sequence 3648, App Sequence 4199, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 3, Appl Sequence 13, Appl Sequence 8, Appl Sequence 18, Appl Sequence 18, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl
2 US-10-108-511-5 2 US-10-108-511-2 2 US-10-1210-155-5 2 US-10-085-198-72 2 US-10-085-198-72 5 US-10-085-198-70 5 US-10-085-198-70 5 US-10-085-198-70 5 US-10-172-174 5 US-10-15-152-35-34 4 US-10-015-535-28	9 9 9
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## ALIGNMENTS

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Sequence 5, Application US/09819371
Publication No. US20040053344A1
GENERAL INPORMATION:
CENERAL INPORMATION:
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca TITLE OF INVENTION: Using Thereof
TITLE OF INVENTION: Using Thereof
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 274; Conserv
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Sequence 4, Application US/09819371
Publication No. US20040053344A1
Publication No. US20040053344A1
Publication No. US2004005334A1
Publication No. US2004005334A1

APPLICANT: Egawa, Kohji
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of TITLE OF INVENTION: Using Thereof
FILE REPERBNCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT APPLICATION NUMBER: US/09/819,371
NUMBER OF SEQ ID NOS: 6
SOGTWARE: Patentin version 3.0
SEQ ID NO 4
LENGHH: 362
TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Score 1496; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.9e-140;
Matches 274; Conservative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1887
LENGTH: 442
                                                                                                  TYPE: PRT
ORGANISM: Homo_sapiens
                                                                                                                                                  US-10-408-765A-1887
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APPLICANT: Fahy, Eoin D.
APPLICANT: Tahang, Bind B.
APPLICANT: Thang, Bind B.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Marnock Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660089.465
CURRENT APPLICATION NUMBER: US/10/408,765A
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                                                                                                                                                                                     Sequence 82, Application US/10257021
Publication No. US20030211498A1
Seduence 10 No. US20030211498A1
Seduence 10 No. US20030211498A1
SEDERAL INFORMATION:
APPLICANT: Morin, Patrice J.
APPLICANT: Pizer, Ellen S.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER FILE REFERENCE: 14014.0369U2
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: ECT/US01/10947
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1496; DB 12; Best Local Similarity 100.0%; Pred. No. 3.8e-140; Matches 274; Conservative 0; Mismatches 0;
                                                             241 FOKWAAUVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                          FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82
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US-10-408-765A-1887
                                                                                                                                               RESULT 2:
US-10-257-021-82
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APPLICANT: Edinger, Shlomit
APPLICANT: Edinger, Shlomit
APPLICANT: Blerman, Karen
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
APPLICANT: HERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOURERY APPLICANT: 100 NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
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                                                                                                                                                                                                                                                                                                                      61 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                               1 GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDYISINEDLRSWTAADTVAQITQRPYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                           Length 326;
                                                                                                         Indels
                                    79.1%; Score 1184; DB 12;
78.8%; Pred. No. 3.7e-109;
Live 22; Mismatches 36;
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PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 160, Application US/10210172; Publication No. US20040043928A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
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APPLICANT: Miller, Charles
APPLICANT: Patturdian, Meera
APPLICANT: Pena, Carol
APPLICANT: Reger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
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Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Anderson, David
Guo, Xiaojia
                                        Query Match
Best Local Similarity 78.8<sup>†</sup>
Matches 216; Conservative
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Gorman, Linda
Leite, Mario
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Publication No. US20040044182A1

GENERAL INFORMATION:

APPLICANT HUNC, UGAR S.

APPLICANT HUNC, UGAR S.

APPLICANT HUNC, UGAR S.

TITLE OF INVENTION:

TITLE OF INVENTION: US20040044182A1 30772

FILE REFERENCE: Docket No. US20040044182A1 30772

FILE REFERENCE: Docket No. US20040044182A1 30772

FILE REPRENCE: Docket No. US20040044182A1 30772

FILE
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APPLICANT: Rosen et al.

IIILE OP INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA.06

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.6%; Score 1311; DB 9; Length 271;
99.6%; Pred. No. 6.5e-122;
iive 1; Mismatches 0; Indels
262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                        ; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6
Matches 241; Conservative
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US-09-925-301-1431
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CRGANISM: Homo sapiens
US-10-380-880-7
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FR 269
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US-10-380-880-7
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Spaderna, Steven
Voss, Edward
Malyankar, Uriel
Anderson, David
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US-10-093-463-78
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Best Local Similarity
Matches 216; Conservat
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PRIOR FILING DATE: 2001-08-08

PRIOR PLING DATE: 2001-08-08

PRIOR PLING DATE: 2001-08-08

PRIOR PELING DATE: 2001-08-09

PRIOR PELING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 60/311,979

PRIOR PELING DATE: 2001-08-13

PRIOR PELING DATE: 2001-08-13

PRIOR PELING DATE: 2001-08-17

PRIOR PELING DATE: 2001-08-16

PRIOR PELING DATE: 2001-08-17
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78.5%; Score 1174.5; DB 12; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3;
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Publication No. US20030208039A1
GENERAL IRFORMATION:
APPLICANT: Badigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rekuda, Ramesh
APPLICANT: Rekuda, Ramesh
APPLICANT: Paccal
APPLICANT: Rastelli, Luca
APPLICANT: Mazes, Peter
APPLICANT: Maresi, Peter
APPLICANT: Garlach, Valerie
APPLICANT: Garlach, Valerie
APPLICANT: Casman, Stacie
APPLICANT: Casman, Stacie
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Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
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Liu, Xiaohong
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-160
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Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
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APPLICANT:
APPLICANT:
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### PRPLICANT: Anderson, David Applicant: Anderson, David Applicant: Anderson, David Applicant: Miller, Charles Applicant: Miller, Charles Applicant: Miller, Charles Applicant: Tampler, Charles Applicant: Tampler, Charles Applicant: Tampler, Charles Applicant: Tampler, Charles Good, Charles Sood, Charles Sood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDGKDYLALNEDLRSWTAADTAAQISKRKCEAANVAEQRRAYLEGTCVEWLHRYLENGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.5%; Score 1174.5; DB 15; Lengtilarity 78.0%; Pred. No. 4e-108; Conservative 22; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EWTTGYAKANAQTDRVALRNILIRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                 Liu, Xiaohong
Spytek, Kimberly
Gorman, Linda
Spaderna, Steven
Voss, Edward
Malyankar, Uriel
Anderson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-093-463-80
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                                                                                                                                                                                         Sequence 6, Application US/09819371

Publication No. US20040053344A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Cantille DF INVENTION: Using Thereof
TITLE OF UNEMPTION: Using Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAWDGKDYISLNEDLRSWTAADTVAQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI 142
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178 TLORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEOTODTELVETRPAG 237
                      205 MLQRADPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGEDQTQDVELVETRPAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRADPPKAHVAHHPISDHEATLR 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
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                                                                     238 DGTFOKWAAVVVPSGEEQRYTCHVQHEGLPOPLILRW 274
                                                                                        CWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 237
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Sequence 80, Application US/10093463
Publication No. US20030208039A1
GENERAL INFORMATION:
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APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Sevida, Ramesh
APPLICANT: Gusev, Vladimir
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
APPLICANT: Ratelli, Luca
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
Pena, Carol
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Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-819-371-6
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US-09-819-371-6
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Gaps

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Sequence 6, Application US/10073300
Publication No. US2003003535A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATY: Reliter, Yoram
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
CURRENT APPLICATION WINBER: US/10/073,300
CURRENT FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 280
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                        61 EWTIGYAKANAQIDRVALENILERRYNQSEAGSHTLQGMNGCDMGPDGRLLERGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                              85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTLQNMFGCDVGSDWRFLRGYHQYAYDG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KDYISLNEDLRSWIAADTVAQITQRFYBABEYABEFRIYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 KDYIALKEDLIKSWIAADMAAQTIKHKWEAAHVAEQLRAYLEGICVEWLRRYLENGKETIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLINQRDGEEQTQDTELVETRPAGDGT
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                                                                                                                                                                                                                25 GSHSMRYFFISVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEVW
                                                                                                                                                                1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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        Length 365;
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                                                                                      Indels
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76.6%; Pred. No. 3.6e-106;
iive 22; Mismatches 42;
Query Match 77.1%; Score 1154; DB 14; Best Local Similarity 77.0%; Pred. No. 4.1e-106; Matches 21; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fokwaavvvesgoegkyrchvoheglekeltikw 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 FQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FOKWAAVVVPSGEEORYTCHVQHEGLPQPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.6
Matches 210; Conservative
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US-10-073-300-6
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US-10-075-257-6
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             KDYIAINEDLHSWTAANTAAQISQHKWEADKYSEQVRAYLEGKCMEWLRRHLENGKETLQ 204
                                                                                                                                      RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                   205 HADPPKAHVTQHPISDHEATLRCWALGIYPAEITLIWQQDGBDQTQDTELVETRPAGDGT 264
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EXPLICATION OF A STATE OF THE PROPER OF THE PROPERTIES OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/10138888
| Sequence 23, Application US/10138888 |
| Publication No. US2003014897241 |
| Publication No. US2003014897241 |
| Discouration No. US2003014897241 |
| Discouration No. USAPLICANT: Thomas, Winston J. Feder, John N. Gnirke, Andreas Ruddy, David Tsuchihashi, Zenta Wolff, Roger K. TITLE OF INVENTION: Hereditary Hemochromatosis Gente NUMBER OF SEQUENCES: 79 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New
                                                                                                                                                                                                                                                                                                                                                       241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.365
OTHER INPORMATION: /note= "
Class I (MHC) protein"
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 365 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10073300;
Sequence 5, Application US/10073300;
Publication No. US2033003535A1
GENERAL INFORMATION:
APPLICANT Reiter, Yoram
TILE OF INVENTON: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
CURRENT APPLICATION UNMBER: US/10/073,300
CURRENT PILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 415
APPLICANT: Reiter, Yoram
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
TITLE OF INVENTION: CONSTRUCTS ENCODING SAME AND METHODS OF GENERATING SAME
PILE REFERENCE: 02/23338
CURRENT APPLICATION NOWHER: US/10/075,287
CURRENT FILING DATE: 2020-02-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENT NESSOR NOS: 20
LENGTH: 280
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                                                                                                                                                                                                                          77.1%; Score 1153; DB 16; Length 280; 76.6%; Pred. No. 3.6e-106; ive 22; Mismatches 42; Indels 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 76.6%
Matches 210; Conservative
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Best Local Similarity 76.61
Matches 210; Conservative
                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-075-257-6
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US-10-073-300-5
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OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain US-10-075-257-5
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| Sequence 5, Application US/10075257 |
| Sequence 5, Application US/20040086960A1 |
| Sequence 5, Application No. US20040086960A1 |
| GENERAL INFORMATION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES, TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES, TITLE OF INVENTION: CONSTRUCTS ENCODING SAME AND METHODS OF GENERATING SAME CURRENT FILING DATE: 2002-02-15 |
| NUMBER OF SEQ ID NOS: 20 |
| SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 5 |
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236 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQ 295
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                                                                                                     RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWORDGEBOTODTELVETRPAGDGT
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Job time : 52 secs
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ORGANISM: Artificial sequence
PEATURE:
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                                                                                                              181
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OM protein - protein search, using sw model

June 18, 2004, 19:19:06; Search time 18 Seconds (without alignments) 792.623 Million cell updates/sec Run on:

US-09-819-371-5 1496 I GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141581 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	homo sapie	pan	mace	homo	goril	рошо	homo a	homo	homo	homod	goril	homo	рошо		goril	homo	homo	homo	homo	homo	homo	pan t	homo	homo	homo	homo	homo	homo	pan t	homo	homo	pan t	рошо
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P30515 8	P30387 9	P30486 P30386 c	P04222	P16188 }	029963	P30685 1	Q29940 }	P30466 1
1A01_SAGOE 1C02_GORGO	1C04_GORGO 1B82_HUMAN	1B48 HUMAN	1C03 HUMAN	1A30 HUMAN	1C06_HUMAN	1B35 HUMAN	1B59 HUMAN	1B18_HUMAN
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365 366	366 362	362	366	365	366	362	362	362
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1210	1209	1207	1206	1205	1205	1203	1203	1202
34 35	36	99	J 4.	41	42	43	44	45

## ALIGNMENTS

RESULT 1 HIMAP HUMAN STANDARD; PRT; 362 AA.  AC P1051; DT (1-APR-1993 (Rel. 25, Last sequence update) DT 01-APR-1993 (Rel. 25, Last sequence update) DT 01-APR-1993 (Rel. 41, Last annotation update) DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F B antigen) (Leukcoyte antigen P) (CDA12). GN HLA-F OR HLA-5.4. GN HLA-F OR HLA-5.4. OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI TAXLD-9606;	[1] SEQUENCE FROM N.A. Medal688605; MEDLINE-90111605; PubMed=1688605; MEDLINE-90111605; PubMed=1688605; Geraghty D.E., Wei X., Orr H.T., Koller B.H.; Geraghty D.E., Wei X., Orr H.T., Koller B.H.; a class I coding sequence linked to a novel transcribed repetitive element."; LEXP. Med. 171:1-18(1990). [2 SEQUENCE FROM N.A. [2 SEQUENCE FROM N.A. [2 SEQUENCE FROM N.A. [3 SEQUENCE FROM N.A. [4 Names N.; The human class I MHC gene HiA-F is expressed in lymphocytes."; The human class I MHC gene HiA-F is expressed in lymphocytes."; and the memonol. 2:531-537(1990).	UENCE FROM N.A. ina S., Tamiya G., Oka A., Ino mo sapiens 2,229,817bp genomic mitted (SEP-1999) to the EMBL/ FUNCTION: Involved in the pre immune system. SUBUNIT: Heterodimer of an al	is SWISS-PROT entry is copyright. It is produced tween the Swiss Institute of Bioinformatics an e European Bioinformatics Institute. There are by non-profit institutions as long as its diffied and this statement is not removed. Usage titles requires a license agreement (See http://send an email to license@isb-sib.ch).	7.1; 7.1; -F. class 19-1; 19_c1
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FUNCTION: Involved in the presentation of foreign antigens to the
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                                                                                                                                                    EMBL, M30685, AAA87973.1; -
HSSP, Q30201; 1A6Z.
InterPro; IPR007310; 1g-like.
InterPro; IPR003006; 1g-MHC.
InterPro; IPR003006; 1g-MHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00147; ig; 1.
Pfam; PF00147; ig; 1.
PFNNTS; PR01638; MHC_I.
PRNTS; PR01638; MHC_I.
PROSTTE; PS000050; MHC_I; 1.
PROSTTE; PS000050; MHC_I; 1.
PROSTTE; PS00290; IG_LIKE; 1.
PROSTTE; PS00290; IG_LIKE; 1.
PHOST I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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Best Local Similarity 98.5
Matches 270; Conservative
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107
346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEGIQDTELVETRPAGDGT 261
                                                                                                                                                                                                                                                                                                                            1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                           22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHIA class I histocompatibility antigen, CH28 alpha chain precursor.
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                       CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BBDD041F820A34E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDILIBE-88319000; PubMed=1412487; MEDILIBE-88319000; PubMed=1412487; Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.; "HLA-A and B polymorphisms predate the divergence of humans and
                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                               DB 1; Length 362;
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90201944; PubMed=1690682;
Lawlor D.A., Warten E., Ward F.E., Parham P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
                                                                                                                                                                                                                                                                            100.0%; Score 1496; DB 1
100.0%; Pred. No. 4e-113;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POKWAAVVVPSGEBORYTCHVQHEGLPQPLILRW 295
InterPro; IPR001039; MHC_I.
Pfam; PF001047; ig; 1.
Pfam; PF001029; MHC_I: 1.
Prom; PF001029; MHCCLASSI.
ProDom; PE000050; MHC_I; 1.
SMART; SM00407; IGG_I; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00835; IG LIKE; 1.
RGATL 1. Transmembrane; Glycoprotein; Signal.
SIGNAL
CHAIN 22 362 HIACLASS I HISTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 AA
                                                                                                                                                                                                                                                        40568 MW;
                                                                                                                                                                                                                                                                                                     Matches 274; Conservative
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Nature 335:268-271(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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2003
3005
3005
1005
1005
1005
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204
204
206
3306
122
122
1024
362 AA;
                                                                                                                                                                                                                                                                                           Local Similarity
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ID 1C28_PANTR
AC P16215;
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DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 ERTIGYAKANAQIDRVALRNILKRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 KDYISLNEDLRSWTAADTVAQITQRPYEAEEYAEBFRTYLEGECLELLRRYLENGKETLQ 201
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203 EXTRACELLULAR ALPHA-2.
295 EXTRACELLULAR ALPHA-2.
305 CONNECTING PEPTIDE.
329 CYTOPLASMIC TAIL.
185 BY SIMILARITY.
280 BY SIMILARITY.
107 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
A; 39084 MW; F83E882D5C2E0971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
immune System.
-1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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Pred. No. 3.8e-111;
1; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
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HLAF MACKU
ID HLAF MACKU
AC P33617;
DT 01-FEB-1994 (
DT 15-JUL-1999 (
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"Structural analysis of an HLA-B27 functional variant: identification of residues that contribute to the specificity of recognition by cytolytic T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398 (1985).
   LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-361 FROM N.A. (B*2701).
MEDLINE=86149317; PubMed=3485286;
Szocts H., Ricthmu-ller G., Weiss E., Meo T.;
"Complete sequence of HLA-187 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (B*2701 AND B*2702).
MEDLINE=86220133; PubMed=3011411;
Seemann G.HA., Rein R.S., Brown C.S., Ploegh H.L.;
Gene conversion-like mechanisms may generate polymorphism in human "Gene I genes";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-007-1986 (Rel. 02, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last annotation update)
14.0-OCT-2003 (Rel. 42, Last annotation update)
15.0-CT-2003 (Rel. 42, Last annotation update)
16.0-CT-2003 (Rel. 42)
17.0-CT-2003 I histocompatibility antigen, B-27 alpha chain precursor
17.0-CT-2003 I antigen B*27)
17.0-CT-2003 (Rel. 2003)
17.0-CT-
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                                                                                                                                                                                                                                                                                                                                                                                       1B27 HUMAN STANDARD; PRT; 362 AA.
P03989; P10317; P10318; P19373; P30467; Q08136; Q29693; Q29846;
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Ezquerra A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96086486; PubMed=7482496;
Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (B*2701).
MEDLINE=86138405; PubMed=3912316;
Weiss E.H., Kuon W., Doerner C., Lang M., Riethmueller G.;
"Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations.";
Immunobiology 170:367-380(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vega M.A., Ezquerra A., Rojo S., Aparicio P., Bragado R.,
Lopez de Castro J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "On the nucleotide sequences of B*2702 and B*2705.";
Tissue Antigens 46:50-53(1995).
                                                                                                                                                                                    262 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPQPLTLRW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -C allelic series.";
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986)
                                                                                                                                               239 GIFOXWAAVVVPSGEEORYICHVOHEGLPOPLILRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 86-107 AND 171-181 (B*2702).
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MEDLINE=88227491; PubMed=3286582;
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Biochemistry 24:1733-1741(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 25-295 (B*2701).
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EMBO J. 5:547-552(1986).
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Lopez de Castro J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary
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1827 HOMAN
1827 HOMAN
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1939991
19-0CT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 38:141-145(1993).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
HLA class I histocompatibility antigen, alpha chain F precursor (HLA antigen) (Leukocyte antigen F).
HLA-F OR HLAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system. SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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SIMILARITY.

HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.

STRACELLULAR ALPHA-1.

SEXTRACELLULAR ALPHA-2.

SEXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                              Otting N., Bontrop R.E., "Characterization of the rhesus macaque (Macaca mulatta) equivalent of \mathrm{HLA}\text{-}\mathrm{F.''};
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1416; DB 1; Length 348;
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94.9%; Pred. No. 1e-106;
tive 4; Mismatches ?
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InterPro; IPR001597; Ig_c1.
InterPro; IPR001597; Ig_c1.
InterPro; IPR0010306; Ig_MG_I.
Pfam; PP00129; MHC_I.
Pfam; PP00129; MHC_I.
ProDom; PP00129; MHC_I.
PRINTS; PR01638; MHCCI.
ProDom; PR01638; MHCCI.
ProDom; PR01638; IG_LI.
PROSITE; PS00290; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
MHC_I; Transmembrane; Glycoprote
                                                                                                              Macaca mulatta (Rhesus macaque)
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HSSP, Q30201; 1A6Z.
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SEQUENCE FROM N.A.
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MEDLINE=22344622; PubMed=12244049;
Hulemeyer M., Hillig R.C., Volz A., Ruhl M., Schroder W., Saenger W., Ziegler A., Uchanska-Ziegler B.;
HLA-B7 subtypes differentially associated with disease exhibit subtle structural alterations.";
J. Biol. Chem. 277:47844-47853(2002).
                                                                                                                                                                                                                                                                                                                                                                    Choo Y.S., Fan L.A., Hansen J.A.;
"A novel High-227 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.";
J. Immunol. 147:174-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a novel HLA-B27 subtype by restriction analysis of a cytotoxic gamma/delta T cell clone."; J. Immunol. 153:3093-3100(1994).
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SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95148615; PubMed=7846047;
Rognan D., Scapozza L., Folkers G., Daser A.;
Rational design of nonnatural peptides as high-affinity ligands for the HLA-B*2705 human leukocyte antigen.";
Proc. Natl. Acad. Sci. US.A. 92:753-757(1995).
Choo S.Y., St John T., Orr H.T., Hansen J.A.;
"Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703)
identifies a unique single amino acid substitution.";
Hum. Immunol. 21:209-219 (1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY.
MEDLINE=92018187; PubMed=1922337;
Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
"The structure of HLA-B27 reveals nonamer self-peptides bound in sextended conformation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
MEDLINE=92405152; PubMed=1525820;
Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
The three-dimensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC.";
Cell 70:1035-1048(1992).
                                                                                       SEQUENCE FROM N.A. (B*2704 AND B*2706).
MEDLINE=56134006; PubMed=8550101;
Rudwalleit M., Bowness P., Wordsworth P.;
"The nucleotide sequence of HLA-B*2704 reveals a new amino acid substitution in exon 4 which is also present in HLA-B*2706.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95064789; PubMed=7974468;
Hildebrand W.H., Domena J.D., Shen S.Y., Marsh S.G.E., Bunce N
Guttridge M.G., Darke C., Parham P.;
"The HLA-B7Qui antigen is encoded by a new subtype of HLA-B27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                       MEDLINE=94102824; PubMed=8276469; Vilches C., de Pablo R., Kresisler M.; "Nucleotide sequence of HLA-B*2706."; Immunogenetics 39:219-219(1994).
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                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91268545; PubMed=1711072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lissue Antigens 44:47-51(1994).
                                                                                                                                                                                   [mmunogenetics 43:160-162(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (B*2708)
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       -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of B-27 are known:
B*2701=8*2705, B*2702 (B27.2; B-27k; B27e), B*2703 (B27d), B*2704,
B*2706, B*2707, B*2708 (B7Qui) and B*2709 (B27-ci). The sequence shown is that of B*2708 (B7Qui) and the development of ankylosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAI PRMEPREPWVEQEGPQYW
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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EMBL, X03664, CAA27301.1; --
EMBL, X03667, CAA27301.1; JOINED.
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SMART; SM0407; IGG1; 1.
PROSITE; PS00290; IG_INE; 1.
PRO I; Transmembrane; Glycoprote
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25 362 HL2
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Interpro; IPR003597; Ig_c1.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR001039; MHC_I.
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Pfdm, PF00047; ig; 1.
Pfam, PF00129; MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC I; 1.
cwart: SM00407; IG01; 1.
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AACS0444.11
AACS0447.11
CAAS1980.11
AAACS9658.11
AAACS9658.11
CAA833876.11;
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PIR, 156116, 156116.

PIR, 156116, 156116.

PIR, 156116, 156116.

PDB, 11804, 15-OCT-92.

PDB, 11804, 30-SEP-94.

PDB, 11801, 30-SEP-94.

PDB, 11801, 30-SEP-94.

PDB, 11801, 30-SEP-94.

PDB, 11802, 30-SEP-94.
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L38504; AAA69724.1;
M54883; AAA59616.1;
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CAA27302.1;
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U35734; 2
X73578; 0
M62852; 2
L19923; 2
Z33453; 0
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MEDLINE=92078860; PubMed=1744581;
Lawlor D.A., Warren B., Taylor P., Parham P.;
Lawlor dissel major histocompatibility complex alleles: comparison to human and chimpanzee class I.",
J. Exp. Med. 174:1491-1509(1991).
-:- FUNCTION: Involved in the presentation of foreign antigens to the
                              EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                           KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                         RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-B0103 alpha chain precursor.
Gorilla gorilla (Lowland gorilla)
Bukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Ctarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system.
-!- SUBDAIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
4 EXTRACELLULAR ALPHA-1.
6 EXTRACELLULAR ALPHA-2.
8 CONNECTING PEPTIDE.
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Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCLASSI.
ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00395; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, JH0541; JH0541.
HSSP; P03989; JHSA.
InterPro; JR007110; Ig-like.
InterPro; JPR003597; Ig_c1.
InterPro; JPR003597; Ig_C1.
InterPro; JPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X60254; CAA42806.1; -.
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206
208
3308
332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1B03 GORGO
P30381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
TRANSMEM
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1B03 GORGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDYISLNEDLRSWTAADTVAQITQRFYEAEFYRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 RADTPKTHVTHHPISDHBATLRCWALGFYPABITLIWQRDGBDQTQDTELVETRPAGDGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (B*3904).

TISSUB-Peripheral blood;

MEDLINE=95189597; Pubmed=7533753;

Ogawa A., Tokunaga K., Nakajima F., Kikuchi A., Karaki S.,

Kashiwase K., Ge J., Hannestad K., Juji T., Takiguchi M.;

"Identification of the gene encoding a novel HLA-B39 subtype. Two
amino acid substitutions on the beta-sheet out of the peptide-binding
floor form a novel serological epitope.";

Hum. Immunol. 41:241-247(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRRPWVEQEGPQYW
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of
                                                                                                                            -LINKED (GLCNAC. . .) (BY SIMILARITY) 3DEE82572BD81469 CRC64;
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MEDLINE=93131294; PubMed=8420828;
Kato N., Karaki S., Kashiwase K., Mueller C., Akaza T., Juji
Kano K., Takiguchi M.;
"Molecular analysis of HLA-B39 subtypes.";
Immunogenetics 37:212-216(1993).
                                                                                                                                                                                                                                                                       Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (B*3902 AND B*3905).
MEDLINE=95242308; PubMed=7725307;
Adams E.J., Martinez-Naves E., Arnett K.L., Little A.-M.,
Tyan D.B., Parham P.;
"HIA-B16 antigens: sequence of the ST-16 antigen, further of two B38 subtypes and evidence for convergent evolution b*3902.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                            82.1%; Score 1228; DB 1;
82.1%; Pred. No. 1.4e-91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 FQKWAAVVVPSGEEERYTCHVQHEGLPKPLTLRW 298
                                            BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCN
                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362
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hes 225; Conservative
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333
125
227
110
362 AA;
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Ramos M., Postigo J.M., Vilches C., Layrisse Z., Lopez de Castro J.A.; "Primary structure of a novel HLA-B39 allele (B*3909) from the Warao Indians of Venezuela. Further evidence for local HLA-B diversification in South America.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (B*3924).
TISSUE=Peripheral blood;
MEDLINE=22447027; PubMed=12558815;
BEGFfania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;
"Complementary DNA sequence of the HiA-B*3924 allele.";
Eur. J. Immunogenet. 30:11-12(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 10-362 FROM N.A. (B*3908).
MEDLINE=96435470; PubMed=8838356;
Adams E.J., Little A.-M., Arnett K.L., McAuley J.E., Williams R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A. (B*3910).
MEDLINE=97378891; PubMed=9234488;
Vilches C., Bunce M., de Pablo R., Moreno M.E., Puente S., Sanz L.,
Kreisler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The novel HLA-Cw*1802 allele is associated with B*5703 in the Bubi population from Equatorial Guinea."; Issue Antigens 49:644-648(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURNCE OF 26-206 FROM N.A. (B*3912).
MEDLINE=20066996; PubMed=10600013; Marcos C.Y., Moraes J.R.,
Lazaro A.M., Moraes M.E., Marcos C.Y., Moraes J.R.,
Fernandez-Vina M.A., Stastny P.,
"Evolution of HLA-class I compared to HLA-class II polymorphism in Terena, a South-American Indian tribe.";
Hum. Immunol. 60:1138-1149(1999).
                                                                                                                                                                                              Fernandez-Vina M.A., Lazaro A.M., Araujo H.A., Miller S.,
                                                                                                                                                                                                                                                                                                                                                                                                   Wells R.S., Parham P.; "A novel recombinant HLA-B*39 allele (B*3910) in a South African Zulu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 26-206 FROM N.A. (B*3923).
MEDLINE=21160452; PubMed=11260515;
Akebaka T., Kashiwase K., Ishikawa Y., Tanaka H., Shimizu M.,
Kawai S., Akaza T., Takhashi T., Juji T.;
"Allele frequency of HLA-B39 in the Japanese population and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-206 FROM N.A. (B*3912).
MEDLINE=9929758; PubMed=10372543;
Marcos C.Y., Fernandez-Vina M.A., Lazaro A.M., Moraes M.E.,
Moraes J.R., Stastny P.;
"Novel HiA-A and HiA-B alleles in South American Indians.";
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (B*3906).
Zhang L., Ellexson M.E., Hildebrand W.H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kashiwase K.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Three new HLA-B alleles found in Mexican-Americans.";
                                                                                                                                                                             MEDLINE=96387677; PubMed=8795147;
Zhao W., Fernandez-Vina M.A., Lazaro A.M., Araujo
Stastny P., Fernandez-Vina M.A., Lazaro A.M., Araujo
Stastny P., Fernandez-Vina M.A., Lazaro A.M., Araujo
Trissue Antigens 47:435-437(1996).
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MEDLINE=97142356; PubMed=8988545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              issue Antigens 48:595-597(1996).
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                 TISSUE=Blood;
MEDLINE=96435466; PubMed=8838352;
                                                                                                                           Tissue Antigens 46:401-404(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (B*3901).
SEQUENCE FROM N.A. (B*3909).
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                                                                                SEQUENCE OF 60-196 FROM N.A. (B*3907).
MEDILINE-95317819; BubMed=7797264;
MEDILINE-95317819; BubMed=7797264;
De Stefano G., Watkins D.I.;
"HIA.A Blielles of the Cayapa of Ecuador: new B39 and B15 alleles.";
Immunogenetics 42:19-27(1955).
Immunogenetics 42:19-27(1955).
                                                                                                                                                                                                                                                                                                                                     microglobulin).
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- POLYMORPHISM: The following alleles of B-39 are known: B*3901 (B391), B*3902 (B9.2), B*3903, B*3904 (B39N), B*3905 (ST-16), B*3906 (B390), B*3917 (B3910, B*3912 (B3901v), B*3923 (B39022v1) and B*3924. The sequence shown is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-39 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                     immune system.
-!- SUBUNII: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO: GO:0005887; C:integral to plasma membrane; NAS. GO; GO:0030106; F:MHC class I receptor activity; NAS. GO; GO:0030106; F:MHC class I receptor activity; NAS. InterPro; PR007110; Ig-like.
InterPro; PR007107; Ig-like.
InterPro; PR003006; Ig-MHC.
InterPro; PR003006; Ig-MHC.
InterPro; IRR001039; MHC_I.
identification of a novel B39 allele, B*3923.";
Tissue Antigens 57:169-172(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ATSEZZ, AMESSAZZ, EMBL; L42280, AABS1452.1; EMBL; U76394, AABS3108.1; EMBL; U76394, AABS3108.1; EMBL; U76394, AABS3108.1; U15640; BAAR44047.1; PIR, 138876, I38876, I38876, I54314, PIR, I54365, I58850, IS8850, IS8876, IS8876,
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Pfam; PF00129; MHC I; 1.
PRINTS; PR01689; MHCCLASSI.
ProDom; PD000050; MHC I; 1.
SWART; SW00407; IGc1; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotes
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BAC11811.1; -.
AAN63555.1; -.
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EMBL, M94051; AAA52660.1;
EMBL, M94053; AAA52660.1;
EMBL, U04243; AAA53660.1;
EMBL, 136318; AAA73942.1;
EMBL, 122649; AAA69861.1;
EMBL, U29480; AAA59861.1;
EMBL, U29480; AAC32741.1;
EMBL, U29083; AAC32741.1;
EMBL, U52083; AAC32741.1;
EMBL, U56246; AAB59484.1;
EMBL, U56246; AAB59484.1;
EMBL, U56246; AAB59481.1;
EMBL, U56246; AAB59481.1;
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AF428252; AAN63555.1; -
L42280; AAB51452.1; -
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CARBOHYD
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DISULFID
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EWITGYAKANAQTDRVALRNILRRYNOSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                        KDYISLNEDLRSWTAADTVAQITQRFYBAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                                                                                                                                                                                                                       25 GSHSWRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEGPEYW 84
                                                                                                                                                                                                                                                                                                                                    1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=94294981; PubMed=7517584;
Little A.-M., Domena J.D., Hildebrand W.H., Shen S.Y., Barber L.D., Marsh S.G.E., Bias W.B., Parham P.;
"HiA-B67: a member of the HiA-B16 family that expresses the ME1
                                                                                   CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
Y -> D (in allele B*3912).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1867 HUMAN STANDARD, PRT, 362 AA.

(029836; Q29678; Q8SNG5; Q951A6; Q9BD38;

10-OCT-2003 (Rel. 42, Lest equence update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

11-OCT-2003 (Rel. 42, Last annotation update)

12-OCT-2003 (Rel. 42, Last annotation update)

13-OCT-2003 (Rel. 42, Last annotation update)

14. Class I histocompatibility antigen, B-67 alpha chain precursor (MHC class I antigen B*67).

14. Pumo sapiens (Human)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                             Y -> D (in allele B*3912).
/FIId=VAR 016659.
S -> A (in allele B*3904 and allele
B*3912).
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                              Score 1227; DB 1; Length 362; Pred. No. 1.7e-91;
                                                                                                                                                                                                                                                                                               32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perersdorf E.;
"Molecular diversity of HLA-B.";
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (B*6702).
Iglehart B.A., Leffell M.S.;
"HLA-B-C (PECMOCHT-3'UTR).";
Submitted (FEB-2002) to the BMBL/GenBank/DDBJ databases.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOKWAAVVVPSGEEORYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                                                                                                                                              /FTIG=VAR_016421
                                                                                                                                                                                                                                                          82.0%; Score ...., 81.8%; Pred. No. 1.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-205 FROM N.A. (B*6701)
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                                                                                                                                                                                                                                                                               Best Local Similarity 81.8
Matches 224; Conservative
 1114
206
206
3308
332
332
1110
1188
333
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1115
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209
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1110
125
227
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                                                   DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                      DISULFID
DISULFID
VARIANT
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                                                                                                                                                                                           VARIANT
 DOMAIN
DOMAIN
DOMAIN
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1867 HUWAN
10077 H
10-077 DT 10-077
DT 10-077
DT 10-077
DE HIA-8
OS HUA-8
OS HUM-8
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N-LINKED (GLCNAC.

BY SIMILARITY.

E > G (in allele B*6702).

/FIId=VAR_016536.

/FIId=VAR_016537.

N -> E (in allele B*6702).

/FIId=VAR_016537.

N -> E (in allele B*6702).

/FIId=VAR_016537.

N -> E (in allele B*6702).

/FIId=VAR_016539.

/FIId=VAR_016539.

/FIId=VAR_016539.

/FIId=VAR_016539.

/FIId=VAR_016539.

/FIId=VAR_016539.

/FIId=VAR_016540.

T -> A (in allele B*6702).

/FIId=VAR_016540.

FIId=VAR_016540.

Z -> A (in allele B*6702).

/FIId=VAR_016540.

FIId=VAR_016540.

Z -> A (in allele B*6702).

/FIId=VAR_016540.

FIId=VAR_016540.

Z -> A (in allele B*6702).

/FIId=VAR_016540.
[4]
SEQUENCE OF 26-206 FROM N.A. (B*6702).
Baldassarre L.A., Hurley C.K.;
Baldassarre L.A., Hurley C.K.;
Novel HLA-B allele (HLA-B*67012 variant).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                -:- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
-:- SUBCELLIAR LOCATION: Type I membrane protein.
-:- POLYNORPHISM: The following alleles of B-67 are known: B*6701 (B-67LAV) and B*6702. The sequence shown is that of B*6701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3F6A17FC10230F70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-67 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF487379; AAL93257.1; -...
EMBL; AF321835; AAK09378.1; -...
EMBL; AF321834; AAK09378.1; -...
EMBL; AF50196; AAL18235.1; -...
EMBL; AY050195; AAL18235.1; JOINED.
PIR, 159645; 159645.
HSSP; P30460; 1AGD.
Genew; HGNC:4932; HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIN, 142830; ...
InterPro; IRR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MC.
InterPro; IPR001039; MHC_I.
Pfam; PF001047; Ig; I.
Pfam; PF00129; MHC_I:
PRINTS; PR01638; MHCCLASSI.
PRODOM; PD000050; MHC_I; I.
PRODOM; PD000050; MHC_I; I.
PROSITE; PS0035; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
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SIGNAL 1 2
CHAIN 25 36
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Best Local Sim
Matches 224;
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SIGNAL
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                                                 KDYISLNEDLRSWIAADIVAQIIQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ
                                                                              EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                     GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                 Gaps
                                                                                                                                                                                                                                                                                           10-00T-2003 (Rel. 42, Created)
10-00T-2003 (Rel. 42, Last sequence update)
10-00T-2003 (Rel. 42, Last annotation update)
111. class I histocompatibility antigen, B-73 alpha chain precursor
(MHC class I antigen B*73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINES 94299292; PubMed=7517915; Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.; Vilches C., an atypical HIA-B molecule carrying a Bw6-epitope motif variant and a B pocket identical to HIA-B27.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   SECURNCE FROM N.A. (B*7301).

MEDLINE=95026796; PubMed=7524186;
Parham P., Arnett K.L., Adams E.J., Barber L.D., Domena J.D.,
Stewart D., Hildebrand W.H., Little A.-M.;
"The HLA-B73 antigen has a most unusual structure that defines
second lineage of HLA-B alleles.";
Tissue Antigens 43:302-313(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Antigens 61:20-48(2003).
-i- FUNCTION: Involved in the presentation of foreign antigens
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       Pred. No. 1.7e-91;
; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                       FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                         FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                   363 AA
82.18; 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3] SEQUENCE FROM N.A. (B*7301)
                    Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system.
SUBUNIT: Heter
        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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031612;
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       Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-73 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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ID 1808 HUMAN STANDARD; PRT; 362 AA.

AC 980460, 062901, 095740; 098740; P79542; 095369; Q95J00; Q9GJ20;

AC Q9MY78; Q9MY78; Q9TGM2; Q9TQM2; Q9UQTO;

DT 01-APR-1993 (Rel. 25, Created)
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16; Mismatches 34;
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N-LINKED (GLCNAC. .
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIN) 172230, INTERPRETATION IG-11ke. INTERPRETATION IGNOSS 1 IGC1. INTERPRETATION INTERPRETAT
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X77658, CAA44739.1, --
EMBL, L24373, AAA96733.1, --
EMBL, A311601, CAC35319.1, --
PIR, 137512; S42102.
HSSP, P03969, 1HSA.
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SMART, SMO4047, IGG1; 1.
PROSITE; PS50835, IG_LIKE; 1.
PROSITE; PS00290, IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U04787; AAA53175.1; -.
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MIM; 142830; -.
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227
363 AA;
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EMBL;
EMBL;
EMBL;
EMBL;
 Dunckley H.;

Dunckley H.;

Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides

"Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides

(PCR-SSO) detects eight new alleles: B*0807, B*0809, B*1551, B*3529,

B*3532, B*4025, B*5304 and B*5508.";

Tissue Antigens 55:266-270(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-206 FROM N.A. (B*0809; B*0812; B*0813 AND B*0814).
MEDLINE=21276061; PubMed=11380951;
Steiner N.K., Gans C.P., Kosman C., Baldassarre L.A., Edson S.,
Jones P.F., Rizzuto G., Pimtanothai N., Koester R., Mitton W., Ng
Hartzman R.J., Hurley C.K.;
"Novel HIA-B alleles associated with antigens in the 8C CREG.";
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42) Last annotation update)
11-Cales I histocompatibility antigen, B-8 alpha chain precursor
14-B OR HLAB.
                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-206 FROW N.A. (B*0807 AND B*0809).
MEDLINE=20236861; PubMed=10777103;
Kennedy C.T., Dodd R., Le T., Wallace R., Ng G., Greville W.D.,
Kennedy A., Taverniti A., Moses J.H., Clow N., Watson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elsner H.A., Blasczyk R.; "Identification of the novel allele HLA-B*0809 in a Caucasian individual: estimation of allogeneic potential between B*08
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (B*0801).
TISSUB-BLOOd;
COX S.T., McWhinnie A.U., Robinson J., Marsh S.G.E., Paxham Madrigal J.A., Little A.W.,
"Cloning and sequencing full-length HLA-B and -C genes.";
Tissue Antigens 61:20-48(2003).
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"Identification of a new HLA-B*08 variant, B*08NEW.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-206 FROM N.A. (B*0806).
Marcos C.Y., Lazaro A.W., Noreen H., Staetny P.;
"New HIA-B locus allele.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  SEQUENCE FROM N.A. (B*0801).
MEDLINE=89225215; PubMed=2715640;
Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
"Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-206 FROM N.A. (B*0804).
MEDLINE=97473039; PubMed=9331954;
HAPOPE R.J., Bratlie A.D., Schreuder G.M., Hurley C.K.;
"Characterization of a novel HiA-B allele, B*0804, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 116-206 FROM N.A. (8*0809).
MEDLINE=20166355; PubMed=10703615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 33-257 FROM N.A. (B*0804).
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SEQUENCE OF 26-206 FROM N.A. (B*0810).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Antigens 57:373-375(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (B*0801).
                                                                                        Homo sapiens (Human)
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The Submitted (NAR-1999) to the Evel, Cambank/DDBJ databases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 GSHSMRYFDTAMSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEFRAPWIEQEGPEYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                      CLASS I HISTOCOMPATIBILITY ANTIGEN ALPHA CHAIN.
                                                                                                   CYTOPLASMIC TAIL.

N-LINKED (GLCNAC. . .) (BY SIMILARITY)
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 362;
                                                                                                                                  N -> D (in allele B*0810),
F -> S (in allele B*0810),
F -> S (in allele B*0804),
F Tid=VAR O16503,
S -> N (in allele B*0806),
F Tid=VAR O16504,
L -> W (in allele B*0809),
F Tid=VAR O16506,
S -> R (in allele B*0812),
F Tid=VAR O16506,
S -> T (in allele B*0809),
F Tid=VAR O16506,
S -> T (in allele B*0814),
F Tid=VAR O16507,
N -> YH (in allele B*0814),
F Tid=VAR O16519,
N -> D (in allele B*0807),
F Tid=VAR O16519.
                                                                                                                                                                                                                                                                      Y:-S D (in allele B*0814).

/FTId=VAR 016520.

V > E (in allele B*0806).

FTId=VAR 016509.

D > L (in allele B*0813).

/FTId=VAR 016510.

/FTId=VAR 016510.

/FTId=VAR 016511.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism; 3D structure.
SIGNAL 1 24
CHAIN 25 362 HIA CLASS I HISTOCOMPATIBILIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                         EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 1224; DB 1;
larity 81.0%; Pred. No. 2.9e-91;
Conservative 21; Mismatches 31
                                                                                   CONNECTING PEPTIDE
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430
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2008
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Matches 222; Conserv
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339
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2007
2007
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Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,

Madrigal J.A., Little A.-M.;

"Cloning and sequencing [ull-length HLA-B and -C genes.";

Tissue Antigens 61:20-48(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune system.
-:- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
-:- SUBCELLULA: COATION: Type I membrane protein.
-:- POLYMORPHISM: The following alleles of B-42 are known: B*4201 (Bw-42) and B*4202. The sequence shown is that of B*4201.
                                                                                    1B42_HUMAN STANDARD; PRT; 362 AA.
301280; P79555;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
HIA class I histocompatibility antigen, B-42 alpha chain precursor HIA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (B*4202).
MEDLINE=97387746; PubMed=9243763;
Lardy N.M., Otting N., van de Weerd M.J., van de Horst A.R.,
Waal L.P., Bontrop R.E.;
Waal L.P., Bontrop R.E.;
"Full-length cDNA nuclectide sequence of the HLA-B*4202 allele.";
                                                                                                                                                                                                                                   Craniata, Vertebrata, Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00129; MHC I; 1.
PRINTS; PR01639; MHC I; 1.
SMART; SM00407; IGC1; 1.
SMART; SM04407; IGC1; 1.
PROSITE; PS00290; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A. (B*4201).
SEQUENCE FROM N.A. (B*4201).
SEQUENCE 99235215; PubMed=2715640;
Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
"Immunol. 142:3937-3950(1989).
265 FOKWAAVVVPSGEEORYTCHVOHEGLPKPLTLRW 298
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001039; MHC_I.
Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M24034, AAA59667.1; -.. EMBL, U88407, AAC16437.1; -.. EMBL, AJ30194, CAC38393.1; -.. PIR, IG1865, IG1865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (B*4201).
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                                                                                                                                                                                                                        Homo sapiens (Human)
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MIM; 142830;
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HUMAN
                                                      RESULT
1B42_HU
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Glycoprotein; Signal
                                                              Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003006; Ig_MG_I.
Pfam; PP00047; Ig; 1.
Pfam; PP00047; Ig; 1.
PRINTS; PR01638; MG_I.
ProDom; PR001638; MG_I.
ProDom; PR001638; MG_I.
PROSITE; PS00835; IG_LIKE; 1.
PROSITE; PS00290; IG_MGC, 1.
MGC I; Transmembrae; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40170 MW;
EMBL; X60255; CAA42807.1;
PIR; JH0539; JH0539.
HSSP; P03989; 1HSA.
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Best Local S
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DISULFID
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MEDIATE=29.70866; PubMed=1744581;
MEDIATE=29.70866; PubMed=1744581;
Lawlor D.A., Warren E., Taylor P., Parham P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimparatee class I.";
to human and chimparatee class I.";
V. Exp. Med. 174:1491-1509(1991).
-:- FUNCTION: Involved in the presentation of foreign antigens to the
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01-APR.1993 (Rel. 25, Last sequence update)
01-APR.1993 (Rel. 25, Last sequence update)
01-APR.1993 (Rel. 25, Last annotation update)
Class I histocompatibulity antigen, GOGO-B0101 alpha chain precursor.
Gorilla gorilla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCB_TAXID=9595;
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-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                       CYTOPLASMIC TAIL.

N-LINEED (GLCNAC. . .) (BY SIMILARITY).

SY SIMILARITY.

BY SIMILARITY.

Y -> H (in allele B*4202).

Y -> H (in allele CRC64;

C9155AB015DEAIBE CRC64;
                              CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 362;
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                           HLA CLASS I HISTOCOMPAT'S ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
81.8%; Score 1224; DB 1;
Best Local Similarity 81.4%; Pred. No. 2.9e-91;
Watches 223; Conservative 21; Mismatches 30;
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                                                                         microglobulin).
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DOMAIN
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1B01_GORGO
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N-LINKED (GLCNAC. . .) (BY SIMILARITY)
419EEE29817165A4 CRC64;
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P30485; 019555; 077933; 095392; 09GIL3;
P30486; 019555; 077933; 095392; 09GIL3;
O1-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-ACT-2003 (Rel. 42, Last annotation update)
(MHC class I histocompatibility antigen, B-47 alpha chain precursor HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BY SIMILARITY
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOILL ALPHA CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 1223; DB 1; Length 362;
81.8%; Pred. No. 3.5e-91;
ive 17; Mismatches 33; Indels (
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MEDLINE=88152906; PubMed=3557938;
Zemmour J., Ennis P.D., Parham P., Dupont B.;
"Comparison of the structure of HLA-Bw47 to HLA-B13 and its
                                                                                         EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
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ALPHA CHAIN
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Best Local
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1A23 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kosman C.A., Hurley C.K.;
"Novel HLA class I B locus alleles.";
"Novel HLA class I B locus alleles.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-302 FROM N.A. (B*4702).
TISSUE-Peripheral blood;
MEDLINE=97316881; PubMed=9174155;
Fischer GF., Broer E., Fae I., Leitner D., Mayr W.R.;
Fischer sequence analysis of an HLA-B47 variant (HLA-B*4702).";
Tissue Antigens 49:540-542(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20548605; PubNed=11098929; BILLS J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H., BILIS J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H., Hurley C.K.; Morersity is demonstrated in class I HLA-A and HLA-B alleles in Cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-Tissue Antigens 56:291-302(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of B-47 are known: B*4701,
B*4702 and B*4703. The sequence shown is that of B*4701.
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MIM, 142830, -..

MIM, 142830, -..

MICEPEO; IPR001301 Ig -like.

MICEPEO; IPR001306; Ig MC.

MICEPEO; IPR001309; MHC.

MICEPEO; IPR00120; MHC.

REAL, PR00121; MHC.

REAL, PR00121; MHC.

REAL, PR00129; MHC.

REAL, SMART; SMO407; IGC.

REAL, PR00118; PS00290; IG MHC.

REAL, PR00118; PS00290; IG MHC.

REAL, PR00118; PS00290; IG MHC.

REAL, MHC.

REAL, MHC.

REAL, MHC.

MHC.

MIM, 14810COMPATIBILITY A.

MHC.

MHC.
                                                                                                                  TISSUE=Blood;
MEDLINE=22512091; PubMed=12622774;
Cox S.T., McWhinnie A.T., Robinson J., Marsh S.G.E., Parham !
Madrigal J.A., Little A.-M.;
"Cloning and sequencing full-length HLA-B and -C genes.";
Tissue Antigens 61:20-48(2003).
   relationship to 21-hydroxylase deficiency.";
Immunogenetics 27:281-287(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-206 FROM N.A. (B*4703).
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EMBL; AJ308398; CAC33087.2; -
EMBL; AJ25141; CAC17463.2; -
EMBL; Y09118; CAA70335.1; -
EMBL; AF016643; AAB70513.1; -
EMBL; AF016642; AAB70513.1; -
EMBL; AF071764; AAB70513.1; -
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMS.; AF071764; AAC23752.1; JOINED.
                                                                                          SEQUENCE FROM N.A. (B*4701).
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MEDLINE-92104637; PubMed=1729171;
Little A.M., Madrigal J.A., Parham P.;
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).
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P30447; Q9TQF1; Q9TQF8; Q9TQG5; Q9TQM6;
01-APR-1993 (Rel. 25, Created)
10-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 25, Last annotation update)
HIA class I histocompatibility antigen, A-23 alpha chain precursor (HMC class I antigen A*23) (A-9).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 /Fiid=VAR 016474.
T -> N (in allele B*4702 and allele
B*4703).
                                                                                                                                                                                               D -> S (in allele B*4702 and allele B*4703).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1223; DB 1; Length 362; Pred. No. 3.5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE OF 26-206 FROM N.A. (A*2302 AND A*2303).
MEDLINE=20309230; PubMed=10852390;
Blis J., Steiner N.K., Kosman C., Henson V., Mitton W., I
Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                  7FTIG=VAR_016475.

106 107 LR -> RG (In allele B*4702)

7FTIG=VAR_016476.

362 AA; 40571 MW; E3D3E4CBFRC15EAE CRC64;
EXTRACELIULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 PQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
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1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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"Novel HLA-B allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                           25
                                                     61
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                                                                                                       121
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     "Seven novel HLA-A alleles carry previously observed polymorphisms."; Tiseus Antigens 56:51-552(2000).
-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
                                                                                                                   microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLURAR The following alleles of A-23 are known: A*2301,
A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of
                                                                                                       -1. SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTODLASMIC TAIL.
N-LINKED (GLCNAC. .) (BY SIMILARITY)
BY SIMILARITY .
BY SIMILARITY .
                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR00110; Ig-like.
R InterPro; IPR003006; Ig_MC.
R InterPro; IPR001309; MHC_I.
R InterPro; IPR001039; MHC_I.
R Ffam; PP00129; MHC_I.
R Pfam; PP00129; MHC_I.
R PXINTS; PR01638; MHCLI.
R RNART; SN000050; MHC_I; I.
RNART; SN00407; IGC.I.
R RNOSITE; PS00290; IG_MHC; I.
RNOSITE; PS00290; IG_MHC; I.
RNOSITE; PS01290; IG_MHC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
81.8%; Score 1223; DB 1; Length 365;
Best Local Similarity 81.4%; Pred. No. 3.6e-91;
Matches 223; Conservative 19; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y--C (in allele A*2305).
/FTIG=VAR 016606.
K--N (in allele A*2303).
/FTIG=VAR 016607.
L--W (in allele A*2302).
/FTIG=VAR 016608.
/FTIG=VAR 016608.
/FTIG=VAR 016608.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
                         Steiner N.K., Edson S.M., Mitton W., Ng J., Hartzman R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-23 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
     OF 26-206 FROM N.A. (A*2304 AND A*2305).
                                                                                                                                                                                                                                                                                                               , AF137080, AAD33736.1; --
, AF137079, AAD33736.1; JOINED.
, AF102572; AAD28171.1; --
, AF135549; AAD22272.1; JOINED.
, AF135548; AAD22272.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                          AF140859; AAD31878.1; JOINED. 095352; IHHK.
                 MEDLINE=21068830; PubMed=11169246,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40732 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:4931; HLA-A.
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                                           Hurley C.K.;
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DOMAIN
TRANSMEM
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DISULFID
DISULFID
VARIANT
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HSSP;
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Gaps

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144
                                                                                                             KDYISLNEDLRSWTAADTVAQITQRFYEAEBYABBFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                               RADPPKAHVAHHPISDHEATLRCWALGFYPPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                           120
                                                                                                                                                204
         84
                                                               SECUENCE FROM N.A. (B*3701).
MEDLINE=90207291; PubMed=2320591;
Ennis P.D., Zemmour J., Salter R.D., Parham P.;
Rapid cloning of Hal-A,B CDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                           EWTTGYAKANAQTDRVALRNLLRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (B*3704).

TISSUE-Peripheral blood;

MEDLINE=22025782; PubMed=12028544;

BEtefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;

"Complementary DNA sequence of the novel HLA-B*3704 allele.";

Tissue Antigens 59:142-144(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                     1B37 HUMAN STANDARD, PRT; 362 AA.
P18453, 019627; Q95HA3; Q95HA8; Q95HM9; Q9GJ31;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, B-37 alpha chain precursor (MHC class I antigen B*37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microglobulin).
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- POLYMORPHISM: The following alleles of B-37 are known: B*3701,
B*3704 and B*3705. The sequence shown is that of B*3701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22131942; PubMed=12135437;
Pyo C.-W., Han H., Kim T.G.;
"Identification of a new HLA-B allele, B*3705 containing a Bw6
sequence motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECTENCE OF 1-322 FROM N.A. (B*3701).
Hurley C.K., Bei M., Rodriguez S., Johnson A.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                    241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-206 FROM N.A. (B*3704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    saue Antigens 59:335-337(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (B*3705)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRETQISKTNTQTYREDIRTLIRYYNQSEAGSHTIQRMSGCDVGPDGRLLRGYNGFAYDG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KDYISLNEDLRSWIAADIVAQIIQRFYEAEEFRIYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKAHVAHHPISDHBATLRCWALGFYPABITLTWQRDGBBQTQDTBLVBTRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
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                                                                                                                                                                                                                            81.7%; Score 1222; DB 1; Length 362;
81.4%; Pred. No. 4.3e-91;
ive 19; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> N (in allele B*3705).
/FTId=VAR 016408.
LR -> RG (in allele B*3705).
/FTId=VAR 016409.
Y -> H (in allele B*3704).
/FTId=VAR_016410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_016410.
FAB4375F05474725 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA CHAIN
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BY SIMILARITY.

T -> N (in all
                                                                                          EMBL, M32320; AAA36233.1; --
EMBL, AF389378; AAL26324.1; --
EMBL, AF418078; AAL26324.1; --
EMBL, AF284828; AAK82990.1; --
EMBL, AF284826; AAK82990.1; --
EMBL, AF284827; AAK82990.1; JOINED.
EMBL, U11267; AA19227.1; JOINED.
EMBL, AF303102; AAG21400.1; --
EMBL, AF303101; AAG21400.1; --
PIR, C35997; C35997.
HSSP; P03989; 1HSA.
GGENEW; HGNC:4932; HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AA; 40456 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223; Conservative
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DISULFID
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                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-B0102 alpha chain precursor.
Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalaia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TAXID=9595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawlor D.A., Warren E., Taylor P., Parham P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimparatee class I.";
to human and chimparatee class I.";
J. Exp. Med. 174:1491-1509(1991).
-I. FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 CYTOPLASMIC TAIL.

188 BY SIMILARITY.

283 EX SIMILARITY.

110 N.LINKED (GLCNAC. . .) (BY SIMILARITY)

40204 MW, R19EEE2B7CC7BECD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal.

BY SIMILARITY.

CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BOIO2 ALPHA CHAIN.

# EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-3.
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81.8%; Pred. No. 5.1e-91;
ive 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE
                             265 FQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92078860; PubMed=1744581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO138; MHCCLASSI.
PRODOM; PRO00050; MHC_1; 1.
SNART; SM0407; IGG1; 1.
PROSITE; PSS0835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I, Transmembrane; Glycoprote
SIGNAL
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PIR; JH0540; JH0540.
HSSP; P03989; IHSA.
HSSP; P03989; IHSA.
InterPro; IPR007110; Ig_11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0013006; Ig_MHC.
InterPro; IPR001309; HHC_I.
Pfam; PP00147; ig; I.
Pfam; PP00129; MHC_I:
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Best Local Similarity 81.84
Matches 224; Conservative
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362 AA;
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June 18, 2004, 19:22:16; Search time 45 Seconds (without alignments) 1921.155 Million cell updates/sec
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1496
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                    1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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1: sp archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp human:*
5: sp_invertebrate:*
6: sp mammal:*
7: sp_mhc:*
7: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vortebrate:*
14: sp_unclassified:*
15: sp_vortebrate:*
16: sp_bacteriap:*
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18: sp_vortebrate:*
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14: sp_unclassified:*
15: sp_vortebrate:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q861f0 homo sapien	Q861e9 homo sapien	Q8wlp5 homo sapien	Q95hc0 homo sapien	Q8mgq1 homo sapien	Q9tp68 homo sapien		Q7yr27 pan troglod			078189 homo sapien	Q29705 homo sapien	Q9mw41 macaca mula	_	Q29934 homo sapien	Q9mxi2 pan troglod
SUMMARIES			QI	Q861F0	Q861E9	QSWLPS	Q95HC0	Q8MGQ1	Q9TP68	Q95IT2	Q7YR27	019692	P79612	078189	Q29705	Q9MW41	Q9MXK1	Q29934	Q9MX12
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		Query	Length	324	324	346	442	346	362	346	362	274	362	362	362	354	362	359	362
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			Score	1496	1496	1496	1496	1491	1491	1477	1477	1240	1240	1240	1239	1237	1237	1236	1235
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17	18	61	50	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

100.0%; Score 1496; DB 7; Length 324;

Query Match

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KDYISLNEDLRSWTAADTVAQITQRFYBAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                               198 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
"Hila-E, F, and G polymorphism: genomic sequence defines new variation
spanning the nonclassical class I genes.";
Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He X., Liu Y., Xu L., Zeng Y.; "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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Pred. No. 2.9e-122;
                                                                                                                                                                                                                                             241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                    258 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
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EMBL; AY253269; AA086773.1; --
EMBL; AY253270; AA086774.1; --
GO; GO:0016925; C:membrane; IEA.
GO; GO:0016955; P:immune response; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR001109; Ig-like.
InterPro; IPR00139; MHC.I.
Pfam; PF001047; ig; 1.
Pfam; PF001047; ig; 1.
Pfam; PF001059; MHC.I.
ProDom; PD000050; MHC.I.
PROSITE; PS00229; CRYSTALLIN_BETAGANWA; 1.
PROSITE; PS00229; IG_MHC; I.
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Q8WLP5
Q8WLP5
Q8WLP5
Q1 Q1-MAR-2002 (TrEWBLrel. 20, C3
Q1-MAR-2002 (TrEMBLrel. 20, L6
Q1-OCT-2003 (TrEMBLrel. 25, L6
MHC class Ib antigen.
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AAM74985.1;
AAM74988.1;
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AAM74990.1;
AAM74991.1;
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Best Local Similarity
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AF523295;
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AF523290;
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                                                                                                                                                                                                                                                                                                                                                         KDYISLNEDLRSWTAADTVAQITQRFYEAREYABEFRTYLEGECLELLRRYLENGKETLQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 257
                                                                                                                                                                                                EWTIGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                             EWITGYAKANAQIDRVALRNILRRYNQSBAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 137
                                                                                                                                                                                                                                                                                                            KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                  18 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGEQYW 77
                                                                                                                                                                                                                                                                                                                                                                                                                           RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu Y., Xu L., Zeng Y., He X.;
Liu Y., Xu L., Zeng Y., He X.;
"A new polymorphism in non-classical MHC class I HLA-F.";
Submitted (JAN-2003) to mon-classical MHC class I HLA-F.";
Submitted (JAN-2003) AAO34407.1;
EMBL, AY21102, AAO34407.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016025; P:immune response; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig-MHC.
InterPro; IPR001399; MHC_I.
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324 AA; 36518 MW; E3E028177D2716F4 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (Fragment).
   2.6e-122;
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Pred. No. 2.6; Mismatches
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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100.0%;
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Pfam; PF00129; MHC I; 1.
PRINTS; PR01639; MHCCLASSI.
ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGC1; 1.
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Best Local Similarity
Matches 274; Conserv
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RP SECUENCE FROM N.A. Williams L.M., Moore Y., Geraghty D.E.;

RT Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;

RT Spanning the nonclassical class I genes."

RT Spanning the nonclassical class I genes."

C. Submitted (JUN-2002) to the RMBL/GenBank/DDBJ databases.

C. I. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE CONTROL OF SYSTEM OF THE RESENTATION OF FOREIGN ANTIGENS TO THE CONTROL OF SYSTEM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EWTTGYAKANAQTDRVALRNILIRRYNQSEAGSHTLQGMNGCDMGFDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPABITLIWQRDGEEQTQDTELVETRPAGDGT 240
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142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                                              RADP PKAHVAHHP I SDHEATLRCWALGFYPAE I TL TWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Last annotation update)
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Pred. No. 7.9e-122;
0; Mismatches 1;
                                                                                                                                                                                                           POKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                     241 FOXWAAVVVPSGEEORYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                  346 AA.
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Les 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-0CT-2002 (TrEMBLrel.
01-0CT-2003 (TrEMBLrel.
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HLA-F.
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QBMGQ1;
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Matches
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                                                                                                                   GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
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        Gaps
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to major histocompatibility complex, class I, F.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Strausberg R.;
Submitted (UNN-201) to the EMBL/GenBank/DDBJ databases.
Strausberg IRRO0355; Primmune response; IEA.
InterPro; IRRO0355; Primmune response; IEA.
RINTERPRO; IRRO0356; IG-11ke.
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100.0%; Pred. No. 4.1e-122;
ive 0; Mismatches 0;
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        Mismatches
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Pfam; PP00129; MHC I; 1.
PRINTS; PR01639; MHC I; 1.
SNART; SM0407; IGc1; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00229; IG_MHC; 1.
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        274; Conservative
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SEQUENCE FROM N.A.
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01-OCT-2003 (
Class Ib.
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01-DEC-2001 (
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                                                                                                                                                                                                                                                                                            Williams S.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE MICROGLOBULIN (BY SIMILARITY).

-!-GUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROSTA); CAR46621.1; -...

MICROGLOBULIN (BY SIMILARITY).

BENEL, ALO22723; CAR46621.1; -...

GO, GO:0016021; Caintegral to membrane; IEA.

GO, GO:0016021; Caintegral to membrane; IEA.

GO, GO:0016021; IAC.

FIREPRO; IPRO10164; Crystallin.

BIT ERPED: IPRO10164; Crystallin.

BIT INTERPRO; IPRO1039; MHC_I.

BRANT PRO10129; MHC_I.

BRANT; SMO0407; IGA1.

BRANT; SMO0407; IGA1.

BROSITE; PSO0225; CRYSTALLIN_BETAGAMMA; 1.

BROSITE; PSO0235; IG_MHC; 1.

BROSITE; PSO0235; IG_MHC; 1.
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261
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RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
DJ377H14.9 (Major histocompatibility complex, class I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA; 40578 MW; 970D072C813A07E2 CRC64;
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                          FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                        FOKWAAVVVPPGEEQRYTCHVQHEGLPQPLILRW
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SEQUENCE 362 AA; 40578 M
                                                                                                                 PRELIMINARY;
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Matches 273; Conserv
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Q9TP68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEFRTYLEGECLELLRRYLENGKETLQ 201
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                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       major histocompatibility
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                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Bukazyota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
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Last annotation update)
                                            Created)
Last sequence update)
Last annotation update)
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99.3%; Pred. No. 1.3e-120;
ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21291697; Parham P.;
Adams E.J., Parham P.;
Adams E.J., Parham P.;
Adams E.J., Parham P.;
Genomic analysis of common chimpanzee major hi
complex class I genes.";
Immunogenetics 53:200-208(2001).
EMBL; ARX37493.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro: IPR001064; Crystallin.
InterPro: IPR001064; Crystallin.
InterPro: IPR0010397; Ig_cl.
InterPro: IPR0010397; Ig_cl.
InterPro: IPR0010399; MHC_I.
Pfam; PF00129; MHC_I.
Pfam; PF00129; MHC_I.
PROSITE; PS00255; CRYSTALLIN_BETAGAMMA; I.
PROSITE; PS00229; IG_LIKE; I.
PROSITE; PS00229; IG_LIKE; I.
PROSITE; PS00229; IG_LIKE; I.
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346
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(TrEMBLrel. 25, Last sequ
(TrEMBLrel. 25, Last anno
PRT;
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                                            (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.3
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
PRELIMINARY;
                                                                                                                    MHC class I antigen.
PATR-F.
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Hasegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,
Kondo S., Tokunaga K.;
Kondo S., Tokunaga K.;
Molecular characterization of a novel HLA-B27 allele.";
Molecular characterization of a novel HLA-B27 allele.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
Incorp. Involved IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INCORD STREAM (BY SIMILARITY).
--- SUBDINT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MCROGLOBULIN) (BY SIMILARITY).
--- SUBDINT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MCROGLOBULIN) (BY SIMILARITY).
REMEL; D83049; HAA.
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016055; P:immune response; IEA.
RI InterPro; IPR003006; Ig—IMFC.
RI InterPro; IPR003006; Ig—MFC.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                  0C9A7A4902383219 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Score 1240; DB 7;
8; Pred. No. 4.6e-100;
14; Mismatches 33;
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                                                                            Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; P0000050; MHC I; 1.
SNART; SN00407; IGcl. II.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS508050; IG_MHC, 1.
INON TER I 1 1
NON TER 274 SA5; 31659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      31659 MW;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
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03,
25,
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227; Conservative
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01-MAY-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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HLA-B.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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                                                                                                                                                                                  MEDLINE-22709134; PubMed=12799463; MEDLINE-22709134; PubMed=12799463; Anzai T., Shilna T., Kimura N., Yanagiya K., Kohara S., Shigenari A., Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T., Meyer A., Ikco K., Goljobori T., Bahrama S., Infok H., Meyer A., Ikco K., Goljobori T., Bahrama S., Infok H., "Comparative sequencing of human and chimpanee MHC class I regions unveils insertions/deletions as the major path to genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                 Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             divergence.";
Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
Embl. Abloo087; BaC78191.1; -
SEQUENCE 362 AA, 40625 MW; BAS699D08181A1FF CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0006955; P:immune response; IEA. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B protein (Fragment).
HLA-B.
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                                                                                                                                NCBI_TaxID=9598;
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Matches 272;
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121 KDYIALNEDLSSWTAADTAAQITQRKWEAARVABQLRAYLBGECVEWLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                         181 RADPPKTHVTHHPISDHBATLRCWALGFYPABITLTWQRDGBDQTQDTELVETRPAGDRT
                                                                                                                                                  1 GSHSMRYFHISVSRPGRGEPRFIIVGYVDDILFVRFDSDAASPREEFRAPWIEGEGFEYW
                                                                                                                                                                                                                                   61 EWTIGYAKANAQIDRVALRNILIRRYNQSEAGSHTLQGWNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                    121 KDYISLNEDIRSWTAADTVAQITQRFYEAEBYABEFRTYLEGGECLELLRRYLENGKETLQ
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                                                                                                                GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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Length 274;
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BC00FC372955711D CRC64;

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362 AA; 40486 MW;
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MEDLINE=98427840; PubMed=9756409;
MEDLINE=98427840; PubMed=9756409;
MEDLINE=98427840; PubMed=1.A.;
Novel polymorphism detected in exon 1 of HLA-B*2713.";
Tissue Antigens 52:187-189(1998)
-1 FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMINE SYSTEM (BY SIMILARITY)
-1 SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
EMBL; ARC02618; AAC42275.1; -
HSSP; P03989; 1HSA
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                       362 AA; 40441 MW; 3CA65547E65FDF84 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                    82.9%; Score 1240; DB 7; 1
82.5%; Pred. No. 6.8e-100;
live 18; Mismatches 30;
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InterPro; IPR003597; Ig-11.
InterPro; IPR001039; MHC. InterPro; IPR001039; MHC. InterPro; IPR001039; MHC. I. Pfam; PF000429; MHC. I; I. PR001039; MHC. I; I. PR1NTS; PR01638; MHCLASSI. PR000050; MHC. I; I. SWART; SM00407; IG-I; I. PR0SITE; PS00299; IG-IKE; I. PROSITE; PS00299; IG-MHC; I.
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                                                                                                                            PROSITE; PSC0835; IG LIKE; 1.
PROSITE; PSC0290; IG MHC; 1.
Glycoprotein; Transmembrane.
SEQUENCE 362 AA; 40441 MM;
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01-NOV-1998 (TYEMBLYEL) 08,
01-OCT-2003 (TYEMBLYEL) 25,
MHC Class I antigen.
HLA-B.
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Pfam, PF00129, MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                    Local Similarity 82.5
les 226; Conservative
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                                                                                              25 GSHSWRYFHTSVSRPGRGEPREITVGYVDDTLFVRFDSDAASPREEPRAFWIEQEGPEYW 84
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                                                                                                                                                                                                                                                                                                    181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT
                                                                          1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1015_TaxID=9606;
                                      0
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82.5%; Pred. No. 8.3e-100;
ive 16; Mismatches 32; Indels (
    Length 362;
                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balas A., Santos S., Vicario J.L.; Santos of a novel E "Serological and molecular characterization of a novel E Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
MHC CLASS I ANTIGEN HLA-B.
148B56561595A505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
NOV-10903 (TrEMBLrel. 24, Last annotation update)
HHC class I antigen HLA-B precursor.
82.9%; Score 1240; DB 7;
82.8%; Pred. No. 6.8e-100;
iive 14; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                              241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                al Similarity 82.8
227; Conservative
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Matches 226; Conservative
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25
362 AA;
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77 EEQTRNAKANAQTDRVSLGNLRRYYNQSEGGSHTVQIMYGCDLGPDGRLLRGYHQFAYDG
                                                                                                                    137 KDYIALNEDLRSWTAADMAAQNTQRKWEGDRYAERFRAYLEGRCVEWLRRYLENGKETLQ
                                                                                                                                                                                       RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                      KDYISLNEDLRSWTAADTVAQITQRFYEAEEYABEFRTYLEGECLELLRRYLENGKETLQ
              EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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; Pred. No. 1.2e-99;
15; Mismatches 32;
                                                                                                                                                                                                                                           241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                               257 FOKWGAVVVPSGEBORYTCHVOHEGLPEPLTLRW 290
                                                                                                                                                                                                                                                                                                                                                                              362
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SEQUENCE 362 AA; 40442 MW;
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PROSITE; PS00290; IG MHC; 1.
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82.8%;
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PERM; PF00129; MHC I; 1.
PRINTS; PR010189; MHC I; 1.
PRODOM; PD000050; MHC I; 1.
CMRRT: SM00407; IGC1; 1.
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EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
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                                                                            KDYISLNEDLRSWIAADIVAQIIQRPYBABEYAEBFRIYLEGECLELLRRYLENGKETLO
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SEQUENCE FROM N.A.
MEDLINE-96386644; PubMed=8794394;
VOSS G., Letvin N.L.;
"Definition of human immunodeficiency virus type 1 gpl20 and cyclocoxic T-lymphocyte epitopes and their restricting major cyclocoxic T-lymphocyte epitopes and their restricting major histocompatibility complex class I alleles in simian-human immunodeficiency virus-infected rhesus monkeys.";
J. Virol. 70:7335-7340(1996).
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen Mamu-B*12 (Fragment).
Macaca mulatta (Rhesus macaque).
Eukaryota; Metaxoa; Orocataa; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                 FQXWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                             FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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Pram. PF00129; MHC I; 1.
PRINTS; PR01639; MHCCLASSI.
Pr0D0m; PR000050; MHC_I; 1.
SWART; SW00407; IGC.I; 1.
PR0SITE; P800290; IG_HKE; 1.
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MEDLINE-20322475; PubMed=10866106;

MEDLINE-20322475; PubMed=10866106;

Medrigal J.A., Bontrop R.B.;

Madrigal J.A., Bontrop R.B.;

"Major histocompatibility complex class I diversity in a West African chimpanze population; implications for HIV research.";

Immunogenetics 51:398-409(2000).

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Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                           205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGBDQTQDTELVETKPAGDRT 264
KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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SEQUENCE FROM N.A.
MEDLINE=86149317; PubMed=3485286;
Szots H., Riethmuller G., Weiss E., Meo T.;
Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and -C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allelic series.";
Proc. Natl, Acad. Sci. U.S.A. 83:1428-1432(1986).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLUE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
EMBL, MIGGTE, ARAS9614.1;
--- HSSP; P03989; 1HSA.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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NON TER 1 1
SEQUENCE 359 AA; 40042 MW; 65B534A8980E7A88 CRC64;
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Best Local Similarity 82.5%; Pred. No. 1.5e-99;
Matches 226; Conservative 14; Mismatches 34;
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GO; GO:0006955; P:immune response; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-li.
InterPro; IPR003005; Ig-MEC.
InterPro; IPR001039; MHC_I.
Pfam; PF00147; ig; 1.
Pfam; PF00129; MHC_I. 1.
Pfam; PF00129; MHC_I. 1.
Propom; PR000050; MHC_I. 1.
SMART; SM00407; IGGI. 1.
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PROSITE; PS00290; IG MHC; 1.
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QY 181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240

DD 202 RVDPPKTHVTHHPISDHEATLRCWALGFYPAEITLIWQRDGEDQTQDTELVETRPAGDGT 261

QY 241 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274

DD 262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295

Search completed: June 18, 2004, 19:28:05

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Sequence 187, Appl
Sequence 1431, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 4013, Ap
Sequence 30718, Ap
Sequence 31089, A
Sequence 315, App
Sequence 335, App
Sequence 355, App
                                                                                                    June 18, 2004, 19:31:27; Search time 48 Seconds (without alignments) 1611.540 Million cell updates/sec
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                                                                                                                                                                                                  274
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_RW PUBL_pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_RW PUBL_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUBL_pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUBL_pep:*
6: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-257-021-82

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C US-09-925-3-01-1431

2 US-09-819-371-4

2 US-09-819-371-6

5 US-10-29-386-30718

4 US-10-029-386-30718

4 US-10-029-386-31089

US-10-029-386-31089

US-10-029-386-31089

US-10-029-386-31089

US-10-029-386-31089

US-10-029-386-31089

US-10-10-10-156

2 US-09-925-302-835

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2 US-10-10-1156

2 US-10-10-1156
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Gapop 60.0 , Gapext 60.0
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Maximum DB seg length: 200000000
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Perfect score:
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16   39   19   19   19   19   19   19   19	<b>ᲐᲮᲗᲗᲔᲥᲥᲠᲥᲡᲡᲮᲗᲗᲔᲥᲥᲠᲥᲡᲡᲮᲗᲗᲔᲥᲑᲠᲥᲡ</b>	80 N N N N N N N N N N N N N N N N N N N	Query Mat Best Loca Matches	9 90

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US-10-029-186-31089
US-10-029-186-31089
US-10-029-186-31089
Sequence 31089, Application US/10029386
Publication No. US20030184704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANDAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
LENGTH: 91
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Sequence 835, Application US/09925302

Sequence 835, Application US/09925302

GENERAL INFORMATION:
TITLE DE INFORMATION:
TITLE DE INFORMATION:
CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 835

TYPE: PRI
TYPE: PRI

TYPE: PRI

TYPE: PRI

SEQ ID NO 835
                                                                                                                                                                                                                                            Length 77;
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                                                                                                                                                                                                                                                                                                                                                                  224 QIQDIELVEIRPAGDGIFQKWAAVVVPSGEEQRYICHVQHEGLP 267
                               FEATURE:
COTHER INFORMATION: MAP TO CHR6.1
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
COTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRI

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004204.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P30509; EVALUE 1.00e-52
US-10-029-386-310A
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100.0%; Pred. No. 8.5e-36;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                            Query Match
16.1%; Score 44; DB 14; I
Best Local Similarity 100.0%; Pred. No. 7.3e-36;
Matches 44; Conservative 0; Mismatches 0;
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Matches 44; Conservative
   ORGANISM: Homo sapiens
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Sequence 30718, Application US/10029386
Sequence 30718, Application US/10029386
Sequence 30718, Application US/20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION UNMER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HONGIN BOOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRENOES: AECMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SSCFTWARE: Annomax Sequence Listing Engine vers. 1.1
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4063
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                                                                                                                                                                                                                                                                     1 YAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 60
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                                                                                                                                                         Gaps
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                                                                                      Query Match 25.5%; Score 70; DB 15; Length 186; Best Local Similarity 100.0%; Pred. No. 1.7e-61; Matches 70; Conservative 0; Mismatches 0; Indels
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24.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 9.4e-60;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO CHR6.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.006-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 34273, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                  126 LNEDLRSWIA 135
                                                                                                                                                                                                                                                                                                                                                                  61 LNEDLRSWTA 70
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 KWAAVVVP 250
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LENGTH: 77
TYPE: PRT
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LENGTH: 96
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APPLICANT: ALBORDEON LAI, COULT, COULTER APPLICANTI Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
FILE REPERBENGE: 21402-416 A
CURRENT APPLICATION NUMBER: 60/309,501
PRIOR PAPLICATION NUMBER: 60/309,501
PRIOR PELING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-13
PRIOR PELING DATE: 2001-09-13
PRIOR PELING DATE: 2001-09-19
PRIOR PELING DATE: 2001-09-19
PRIOR PELING DATE: 2001-09-03
PRIOR PELING DATE: 2001-09-03
PRIOR PELING DATE: 2001-09-03
PRIOR PELING DATE: 2001-08-03
PRIOR PELING DATE: 2001-08-03
PRIOR PELING DATE: 2001-08-07
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14.6%; Score 40; DB 14; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.3e-32;
Matches 40; Conservative 0; Mismatches 0; Indels
EXPRESSED IN PLACENTA, SIGNAL = 48
EXPRESSED IN FETAL LIVER, SIGNAL = 11
EXPRESSED IN LUNG, SIGNAL = 57
GWISSPROT HIT: P30507, EVALUE 7.00e-24
                                                                                                                                                                                                                                                                            228 TELVETRPAGDGTFOXWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                          29 TELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 68
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PRIOR APPLICATION NUMBER: 60/312,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 156, Application US/10210172 Publication No. US20040043928A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
Boldog, Perenc
Gorman, Linda
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MacDougall, John
Stone, David
Alsobrook II, John
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Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hjalt, 1010
Rastelli, 1uca
Spytek, Kimberly
Edinger, Shlomit
Ellerman, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leite, Mario
Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhous,
Gerlach, Vare
Tord
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     OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: S
                                                                                                                    US-10-029-386-30752
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US-10-210-172-156
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APPLICANT:
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APPLICANT: Rank, David R.
APPLICANT: Penn, Sharron G.
APPLICANT: Parnk, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: PARCEL ADVIDED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGTH: 78
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THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                              FEATURE:

NAME/KEY: SITE

LOCATION: (95)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835
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Sequence 835, Application US/09925302

Publication No. US20030064072A9

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

ITLE OF INVENTION:

TILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: DS01-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 835

LENGTH: 104
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                                                                                                                                                                                                            Length 104
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                                                                                                                                                                                                                                                                                                                     224 OTODIELVETRPAGDGIFOKWAAVVVPSGEEORYICHVOHEGLP 267
                                                                                                                                                                                                         Query Match
16.1%; Score 44; DB 9; Length 104
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   32 OTODIELVETRPAGDGTFOKWAAVVVPSGGEGRYTCHVQHEGLP 75
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OTHER INFORMATION: MAP TO CHR6.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                       ORGANISM: Homo sapiens
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Best Local Similarity
Matches 44; Conserv
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LOCATION: (95)
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US-09-925-302-835
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Sequence 72, Application US/10085198

Publication No. US2004000997A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 21402-279

CURRENT PELLING DATE: 2002-02-25

CURRENT PELLING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/271,646

PRIOR PELLING DATE: 2001-03-16

PRIOR PELLING DATE: 2001-03-16

PRIOR PELLING DATE: 2001-03-16

PRIOR PELLING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/311,981

PRIOR PELLING DATE: 2001-08-13

PRIOR PELLING DATE: 2001-08-13

PRIOR PELLING DATE: 2001-08-16

PRIOR PELLING DATE: 2001-08-20

PRIOR PELLING DA
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PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SEQ ID NO 156
LENGTH: 371
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14.6%; Score 40; DB 15; Length 371;
Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 40; DB 12; Length 371; Best Local Similarity 100.0%; Pred. No. 3e-31; Matches 40; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 TELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 TELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 289
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Job time: 49 secs
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-085-198-72
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LENGTH: 371
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Human pro HLA-G rec Human Pro

Human NOV Human NOV

Human pep HLA-G alp HLA-G rec

Peptide

Peptide #
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Protein #

Adu79455 HLA-G r Adu65494 Human p Adu66572 Human p Ade46572 Human N Ade40254 Human N Adm15751 Peptide Abb29570 Peptide Abb29570 Peptide Abb29570 Peptide Abb29570 Peptide Abb29570 Peptide Abb29570 Peptide Abb29570 Peptide Abb29576 Human b Amm65849 Human b Amm65849 Human b Abg49576 Human n Amm6549 Feptide Abg37468 Human n Amm6775 Human n

Human bra Human liv Peptide

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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer cell specific HLA-F antigen SEQ
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AAMO 5976
ABG40192
AAU79 152
AAU79 153
AAU79 153
ADB65494
ADD46572
ADD46572
ADD46572
ADB7029494
ADD167751
ABB3 140
ADB3 140
ABB2 160
ABB2 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG64618 standard; protein; 274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-00279566.
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    WPI; 2001-360493/38.
N-PSDB; AAH45556.
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MEDINET KK.
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Best Local Simi
Matches 274;
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    AAG64618;
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Abb43986 Human can
Aag642091 Human can
Aag64291 Human sec
Abp42991 Human sec
Abb42991 Lungan ova
Aab8497 Lungan ova
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Aav13283 Novel hum
Aab97793 Human she
Ad631177 Human dia
Ad631177 Human dia
Ad631410 Peptide #
Abb37410 Peptide #
Abb37410 Peptide #
Abb3168 Peptide #
Abb3168 Peptide #
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Aam58091 B
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Compugen Ltd.
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                           GenCore version
Copyright (c) 1993 - 2004
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AAAG02209
AAAB58497
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AAR70391
AAC13073
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AAM58091
ABG52217
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11: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2001s:*
5: geneseqp201s:*
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geneseqp2003bs:*
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                                                                                                             protein search, using
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Maximum DB seq length: 200000000
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EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                                                  120
                                                                                                                   180
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                                                                                                                                                                       240
                                        120
                                                                                           KDYISLNEDLRSWIAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                               KDYISLNEDLRSWIAADTVAQIIQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
                                        EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                 EWITGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                    RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTBLVETRPAGDGT
    Length 362;
                                                                                                                                                                                                                                                                                                                                                               Human cancer cell specific HLA-F antigen SEQ ID
                                                                                                                                                                                               274
                                                                                                                                                                                                                     241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                               FOXWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW
                                                                                                                                                                                                                                                                                                                                                                                         HLA-F antigen, cancer cell specific, human.
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                      AAG64617 standard; protein; 362 AA
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tive 0;
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Best Local Similarity
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA831081-ABA83180, ABA831812, ABA83180, ABA83181 and ABA83184) or segments thereof (MBA83123-ABA83180, ABA83181 and ABA83181). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treaded for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (1.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenoma,
KDYISLNEDLRSWTAADTVAQITQRFYEAEBYABBFRTYLEGECLELLRRYLENGKETLQ 180
                                          201
                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenomi, borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; mucinous cystadenoma; mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; berner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                KDYISLNEDLRSWTAADTVAQITQRFYEAEBYABERRTYLEGECLELLRRYLENGKETLQ
                                                                                                                         RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                      RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT
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mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be everexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and protein of ovarian cancer. Sequences ABBSO257-ABBSO29 represent proteins encoded by ovarian tumour marker genes of the invention
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100.0%; Pred. No. 6.6e-250;
ive 0; Mismatches 0;
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Matches 274; Conservative
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N-PSDB; AAS90913.
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                                                                                                                                                                                                                                                                          Sequence 362 AA;
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23-AUG-2000;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cotivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful artivity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and coil sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the prin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                       Claim 20; SEQ ID NO 57085; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 677 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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AAB43986
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities crissues and calls the genes are expressed in. Example of activities includes cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiametory; antithyroid; antishlergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coaqulant; noctropic; vasorropic; antipaciatic and antiangiogenic. The mortropic; vasorropic; antipaciatic and antiangiogenic. The mortropic; vasorropic; antipaciatic and antiangiogenic. The present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, antiomatic cills, to treat disorders of haematopoietic cells, antiomatic cells, antiomatic cells, and organ rejection, modulate haemostatic or thrombolytic activity, modulate inferential infections. The peptides, mucleotides and organ dantagonists and antagonists may be also be used in the exemplification of the acceptance of the control of the acceptance of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGWNGCDMGFDGRILRGYHQHAYDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDYISLNEDLRSWIAADIVAQIIQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                             comprising sequences encoding peptides
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allergic reaction, graft versus host disease; organ rejection, haemostatic, thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%; Score 241; DB 3; Lr
100.0%; Pred. No. 7.1e-219;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acids comprising sequenuseful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 2115-2116; 2352pp; English
                                                                                                                                                                                 08-MAR-2000; 2000WO-US005882
                                                                                                                                                                                                                   99US-0124270P
                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                        WPI; 2000-587533/55.
N-PSDB; AAC78195.
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                                                                                                            WO200055350-A1
                                                                            Homo sapiens
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                                                                                                                                              21-SEP-2000
                                                                                                                                                                                                                                                                                        Rosen CA,
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Best Local
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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 TORFYBAEEYABEFRTYLEGECLELLRRYLENGKETLORADPPKAHVAHHPISDHEATLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TÕRFYEABEYAEBFRTYLEGECLELLRRYLENGKETLORADPPKAHVAHHPISDHEATLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IAVEXVDDTÇFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 IAVEYVDDIQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTIGYAKANAQIDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRYNOSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 2e-194;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CWALGEYPAEITLIWQRDGEEQTQDTELVETRPAG 237
                                                                                                                                     a
                                                                                                                                     Human cancer cell specific HLA-F antigen SEQ
                                                                                                                                                                               HLA-F antigen; cancer cell specific; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 11-12; 12pp; Japanese.
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AAG64619 standard; protein; 215
                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-00279566.
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es 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EGAW/) EGAWA K.
(MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIMU/) KIMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH45557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 215 AA;
                                                                                                                                                                                                                                                                               JP2001095584-A
                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1999;
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                                                                                           12-SEP-2001
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                                                 AAG64619;
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Matches
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, expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.
                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                         nucleic acid that is a 5' expressed sequence tag (5' EST) for inning cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                            Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
       Human secreted protein, SEQ ID NO: 4290.
                                                                                                        21-FEB-2000; 2000EP-00200610.
                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                               WPI; 2000-500381/45
                                                                                                                                                                                         N-PSDB; AAC00215.
                         Human; 5' EST;
gene therapy;
                                                                                                                                          GEST ) GENSET
                                                                      EP1033401-A2.
                                                                                                                          26-FEB-1999;
                                                    Homo sapiens
                                                                                       06-SEP-2000.
                                                                                                                                                                                                                  obtaining
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genomic DNAs that

Duclert A, Giordano J;

99US-0122487P

The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA primed cDNA libraries. Such ESTs are not well suited for isolating cDNA included. S' ESTs are derived from mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cONAs and genomic DNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors ö 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRREPWVEQEGPQYW 60 81 22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 0; Gaps 36.1%; Score 99; DB 3; Length 120; 100.0%; Pred. No. 3.3e-85; ive 0; Mismatches 0; Indels 61 EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMN 99 99; Conservative Query Match Best Local Similarity Sequence 120 AA; Matches

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; bifertility; pregrancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; Human ovarian antigen HPDRT37, SEQ ID NO:4063. Ä ABP42931 standard; protein; 186 (first entry) 22-AUG-2002 ABP42931; RESULT 8
ABP42931
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cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomedulatory; neuroprotective; antihody ammatory; gynaecological; reproductive. 

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA;

Birse CE,

WPI; 2002-147878/19.

N-PSDB; ABQ56008.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 4063; 2922pp; English

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical comprising human ovarian antigens to the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polymucleotides, antibodies against human ovarian antigens and the use of ovarian antigens prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and catestic tunours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders origin, reproductive system disorders (e.g., infertility, disorders origin, reproductive system cisorders, infertility, disorders origin, reproductive system disorders (e.g., chlamydia, HIV, toxoplammensia, endocrine cisoporystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine cisoporystic ovary syndrome, inflammatory conditions (e.g., mastitis, oophoritis and cysintis), immune disorders (e.g., congenital and acquired to adjoorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and material material disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as therefore madiatives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did neternoric format directly from MIPO cert fire specification, but was obtained in electronic formet directly from WIPO cert fire the printed and the control

Sequence 186 AA;

Gaps ; Length 186; 0; Indels 25.5%; Score 70; DB 5; 100.0%; Pred. No. 1e-57; tive 0; Mismatches 0 Conservative Local Similarity hes 70; Conserva Query Match Best Loc Matches

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126 LNEDLRSWIA 135 ઠે 셤

70 LNEDLRSWIA 61

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Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide corresp. to major histocompatibility antigen regions - used for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.
                                                                                                                                                                                             HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3
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AAP80911 standard; protein; 274 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-00008846.
87US-00138547.
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/note= "al
181. .272
                                                                                                  (first entry)
                                                                              (revised)
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                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1987;
                                                                            25-MAR-2003
18-SEP-1990
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                                      AAP80911;
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                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polymucleotide sequences, their agnists, and antegonists may have neuroprotective; cytostatic; cardioactive; and cantendation in the reaction of the protective; cytostatic; cardioactive; and golymucleotide sequences, their agreeological; or antibacterial cativity. The invention also includes antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide cor polymucleotide sequences. The lung cancer associated polymucleotide cor polymucleotide sequences. The protein or numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as certaiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Sequences and proliferative disorders. The proteins may also be used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
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                                                                                                                                                                                                                                      Human, lung cancer associated protein; neuroprotective, cytostatic, cardioactive; immunoanchilatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibecterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
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                                                                                                                                                                                                    Lung cancer associated polypeptide sequence SEQ ID 835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.1%; Score 44; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.2e-33. Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 1375; 1425pp; English.
                                                                                AAB58497 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US005918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                               14-MAR-2001
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                                                                                                                         AAB584'97;
                                                               AAB5849
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Clayberger C;

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/note= "alpha-3 region"

'note= "alpha-1 region" "alpha-2 region"

Location/Qualifiers

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The concensus sequence is derived from a total of 23 HLA-A,B,C sequences. The protein sequences in the three extrecellular domains (alpha-1, alpha-2 and alpha-3) are shown. The example concerned the effect of peptides from different HLA-A2 epitopes on cytolysis of target cells by CTL of different specificities. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                             16.1%; Score 44; DB 1; Length 274; 100.0%; Pred. No. 4.8e-33; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   224 OTODIELVETRPAGDGIPOKWAAVVVPSGEEORYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                          224 QTQDTELNETRPAGDGTEQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR12466 standard; protein; 366
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(first entry)
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 44; Conservative
                                                                                                                                                                                          Sequence 274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-C exon Cb-2.
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29-AUG-1991
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ID AAR1
XX
AC AAR1
XX
DT 25-P
DT 29-A
DE HLA-
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32 QIQDIELVETRPAGDGIFQKWAAVVVPSGEEQRYICHVQHEGLP 75

RESULT 10 AAP80911

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polypeptides - isolated products for the

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                  The invention relates to a method for disgnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by an uncleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast and encoded.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cytokine; cell proliferation; cell differentiation, gene therapy; vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 26965; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                              16.1%; Score 44; DB 2; Length 366; 100.0%; Pred. No. 6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                     224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                         QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                     New isolated cancer associated nucleic acids and using sera from cancer patients, used to develop diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                                             Disclosure; Page 417-418; 787pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA013073 standard; protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 26965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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             WPI; 1999-132448/11
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                                                                                                                                                                                                                                                                                                          lung cancer
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AAO13073
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                                                                                                                                                                                                                                                                                                                      Probes comprising part of the DNA sequence encoding the protein can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C antigen. See also AAR12455 (same patent) and U03112486 and J03112487. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
Human leukocyte antigen; probe; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                   gene, DNA probe and transformant cells - for immunisation of
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O, Sahin U;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 44; DB 2; Length 366
100.0%; Pred. No. 6e-33;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer associated antigen precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stockert E, Gure A, Cher
Pfreundschuh M, Tureci O,
                                                                                                                                                                                                                                                                     animals and monoclonal antibody development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY07033 standard; protein; 366 AA.
                                                                                                                                                                                                                                                                                               Claim 4; Page 2; 13pp; Japanese
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97US-0061599P.
97US-0061765P.
97US-00948705.
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                                                                                                                                                                                   (OLYU ) OLYMPUS OPTICAL CO LTD
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                                                                                                                            89JP-00247695.
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Obata Y,
                                                                                                                                                                                                              WPI; 1991-182989/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                             N-PSDB; AAQ12117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer.
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10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
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                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998;
                                                                    JP03112485-A.
                                                                                                                            22-SEP-1989;
                                                                                                                                                       22-SEP-1989;
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                                                                                                 14-MAY-1991.
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O'hare M
                 class
                                                                                                                                                                                                                                                       HLA-C
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The invention relates to human polynucleotides (AAI79941-AAI99841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynebtides are useful in gene therspy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, itssue growth factor activity, immunomodilatory activity and activity, inmunomodilatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence date for this patent aid not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              16.1%; Score 44; DB 4; Ls 100.0%; Pred. No. 6.1e-33; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 374 AA;
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Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia. QTQDTELVETRPAGDGTFQKWAAVVVPSGGEEQRYTCHVQHEGLP 299 224 OTODIELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267 Novel human secreted protein #3374. Ź AAU32883 standard; protein; 380 18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160. Tang YT, Liu C, Drmanac RT; 16-APR-2001; 2001WO-US008656 entry) (first (HYSE-) HYSEQ INC WO200179449-A2, Homo sapiens 18-DEC-2001 25-OCT-2001, AAU32883; 256 AAU32883
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proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                          Human; shear stress-response protein; vascular disease; arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequences, proteins encoded by them and antibodies against 'useful in diagnosis and treatment of vascular disease caused by
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                                                                                                                     16.1%; Score 44; DB 4; Length 380
100.0%; Pred. No. 6.2e-33;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.2e-32;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                        AAB90793 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2000; 2000WO-JP006840.
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1es 44; Conservative
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                                                                                           Sequence 380 AA;
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Search completed: June 18, 2004, 19:29:54 Job time : 63 secs

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

WPI; 2001-611725/70.

Claim 20; Page 683-684; 765pp; English.

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Query Match
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## ALIGNMENTS

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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
E Nonolassical MHC class I antigen (Fragment).
B HLA-F.
Submaralia; Eutheria; Drimates; Cararhini; Hominidae; Homo.
NCBI TAXID-9606;
N (1)
E TAXID-9606; NA.
A HE X., Xu L., Liu Y., Zeng Y.;
Nncolassical MHC class I HLA-F.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY216682; AA037689.1; --
COC 00006955; Primmune response; IEA.
COC 00006955; Primmune response; IEA.
COC 00006955; Primmune response; IEA.
R (20) COC 1PR001064; Crystallin.
R InterPro; IPR001064; Crystallin.
R InterPro; IPR001309; MHC I. I.
R Pfam; PF00047; ig; 1.
R PFam; PF00047; ig; 1.
R PROSITE; PS00259; IG LIKE; 1.
R PROSITE; PS00259; IG LIKE; 1.
R PROSITE; PS00259; IG LIKE; 1.
R PROSITE; PS00259; IG LIME; 1.
R PROSITE; PS00259; IG LIKE; 1.
R NON TER 324 AA; 36518 MW; E3E028177D2716F4 CRC64;
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Length 324;

DB 7;

100.0%; Score 274;

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## EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74981.1;
EMBL, AF523295, AAM74992.1;
EMBL, AF523295, EMBL, AF523395, AAM74992.1;
EMBL, AY53269; AAM74992.1;
EMBL, AY53269; AAM866773.1;
EMBL, AY5323970; AAM74992.1;
EMBL, AY5323970; AAM74992.1;
EMBL, AY533296; AAM866773.1;
EMBL, AY533296; AAM866773.1;
EMBL, AY53370; AAM7492.1;
EMBL, AY533296; AM986773.1;
EMBL, AY533296; AM986773.1;
EMBL, AY533296; AM986773.1;
EMBL, AY533290; AM986773.1;
EMBL, AY533290; AM986773.1;
EMBL, AY533290; AM986773.1;
EMBL, AY533209; AM986773.1;
EMBL, AY533290; AM986773.1;
EMBL, AY533390; AM986773.1;
EMBL, AY533390; AM986773.1;
EMBL, AY533390; AM986773.1;
EMBL, AY533390; AM986773.1;
EMBL, AY53
                           KDYISLNEDLRSWTAADTVAQITQRPYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180
                                                               138 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.,
"HLA-E, F, and G polymorphism: genomic sequence defines new variation
spanning the nonclassical class I genes.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            198 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTODTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         He X., Liu Y., Xu L., Zeng Y.; "Cloning of full-length HLA-P*0101 variant 1 cDNA from Han Chinese."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 346;
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Last annotation update)
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Pred. No. 3.3e-279;
                                                                                                                                                                                                                                                      241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                          258 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
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Pfam; PF00129; MHC I; 1.
Probom; PF00150; MHC I; 1.
PROSITE; PS00225; CRYŠTALLIN BETAGAMMA; 1.
PROSITE; PS00225; GRYŠTALLIN BETAGAMMA; 1.
PROSITE; PS002050; IG LIKE; 1.
PROSITE; PS002090; IG MHC; 1.
SEQUENCE 346 AA; 39051 MW; D4782AA4697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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01-MAR-2002 (TrENBLRel. 20, Le
01-OCT-2003 (TrENBLRel. 25, Le
MHC class Ib antigen.
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Best Local Similarity
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                                                                                                                                           181
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Q8WLP5
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                                                                                                                                                                                                  EWITGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                      EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGWNGCDMGPDGRLLRGYRQHAYDG 137
                                                                                                                                                                                                                                                                                                                  KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGGECLELLRRYLENGKETLQ 180
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                                                                                                                                        18 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPPQYW 77
                                                                                        GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRWEPRWEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                   RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAGDGT
                              Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Liu Y., Xu L., Zeng Y., He X.;

Submitted (JAN-2003) to the BMBL/GenBark/DDBJ databases.

Submitted (JAN-2003) to the BMBL/GenBark/DDBJ databases.

BMBL; AV221102; AA034407.1: -

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

InterPro; IPR00110; IG-like.

InterPro; IPR00110; IG-like.

InterPro; IPR00139; IG-l.

R Pfam; PP00047; IG-l.

R Pfam; PP00047; IG-l.

R PRINTS; PR01539; MHC_l: 1.

R SMART; SM00407; IG-l.

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                                 0; Indels
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
   100.0%; Pred. No. 3.1e-279; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
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PROSITE; PSSO835; IG LIKE; 1.
PROSITE; PSO0290; IG MHC; 1.
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01-JUN-2003 (TrEMBLrel. 24, Crea
01-JUN-2003 (TrEMBLrel. 24, Last
01-OCT-2003 (TrEMBLrel. 25, Last
MHC class I antigen (Fragment).
HLA-F.
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Matches 274; Conservative
   al Similarity 100.
274; Conservative
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NON TER
SEQUENCE
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Best Local
Matches 27
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Ishitani A., Miki. A., Williams L.M., Moore Y., Geraghty D.E.;

Ishitani A., miki. A., Williams L.M., Moore Y., Geraghty D.E.;

"HIA-E, F., and G polymorphism: genomic sequence defines new variation
of panning the nonclassical class I genes.";

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
INMUNE SYSTEM (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGOBOLOBILIAN) (BY SIMILARITY).

C.!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGOBOLOBILIANITY).

EMBL; AF523291; AAM74986.1; -..

BMBL; AF532291; AAM74986.1; -..

RMBL; AF532291; Cintegral to membrane; IEA.

GO; GO:0016021; Cintegral to membrane; IEA.

CO; GO:0016021; Cintegral to membrane; IEA.

BRITCHPLO; IPRO0110; Ig-11ke.

INTERPRO; IPRO01306; Ig-MHC.

INTERPRO; IPRO01399; MHC_I:

REPRO; PRO01039; MHC_I:

REPROSED SEARCH AND SEAR
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142 KDYISLNEDLRSWTAADTVAQITQRFYEABEYAEEFRTYLEGECLELLRRYLENGKETLQ 201
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                                                                                  GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 5.6e-254;
ive 0; Mismatches 0;
                                                                                                                                                                                             262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                              241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                      346 AA.
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
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SEQUENCE 346 AA; 39061 MW;
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ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGc1; 1.
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01-OCT-2003 (TERMELTE1, 25
MHC class Ib antigen.
HLA-F.
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Best Local Similarity 100.
Matches 250; Conservative
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Straubberg R.;
Straubberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC009260; AH09260.1; -..
GO; GO:0016621; C:integral to membrane; IEA.
GO; GO:0016925; P:immune response; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig-dt.
InterPro; IPR003306; Ig-MC.
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           Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TEMBLrel. 25, Last annotation update)
Similar to major histocompatibility complex, class I, F.
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Pfam; PF00129; MHC 1; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PF000056; MHC I; 1.
SMART; SM0407; IGC1; 1.
PROSITE; PS00225; CRYSTALLIN BE PROSITE; PS00290; IG LIKE; 1.
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           274; Conservative
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01-OCT-2003
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202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ377H14.9 (Major histocompatibility complex, class
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Pred. No. 5.9e-254;
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100.0%; Pred. No. ...
0; Mismatches
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE 362 AA: 40578 M
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Best Local Similarity 100.
Matches 250; Conservative
                                                                                                                                                                 PRELIMINARY;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Adams E.J., Parham P.;
"Genomic analysis of common chimpanzee major histocompatibility
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Local Similarity 100.0%; Pred. No. 8.1e-210; les 208; Conservative 0; Mismatches 0;
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Immunogenetics 53:200-208(2001).

BMB1, AR318365; AAK779.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0016025; P:immune response; IEA.

InterPro; IPR001064; Crystallin.

InterPro; IPR001010; IG-like.

InterPro; IPR003906; IG_MG.

InterPro; IPR003906; IG_MG.

InterPro; IPR001039; MHC_I.

Pfam; PF00104; ig; I.

Pfam; PF00104; ig; I.

PRMS; PR00105; MHC_I.

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PRODOM; PR00105; MHC_I.

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346 AA
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                                                                 82 EWITGYAKANAQIDRVALRNLERRYNQSEAGSHILQGWNGCDWGPDGRLLRGYHQHAYDG
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MEDLINE=22709134; PubMed=12799463;

MEDLINE=22709134; PubMed=12799463;

MEDLINE=22709134; PubMed=12799463;

Manzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A. Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamazaki M., Taehiro H., Iwanoto C., Umohara Y., Imanishi T., Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H., "Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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66.4%; Score 182; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-182;
Matches 182; Conservative 0; Mismatches 0; Indels
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EMBL: AB100087; BAC78191.1; -.
SEQUENCE 362 Aa; 40625 MW; BA5699D08181A1FF CRC64;
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243
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                                                                                                                                          Gorilla gorilla (gorilla).
Gorilla gorilla (gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
Mombalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                  A Grimsley C.;

A Grimsley C.;

A Grimsley C.;

"Hia-P: A monomorphic locus in an African-American sample.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

R Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

R PRESI, AF159566; AAD51614.1;

R InterPro; IPR003006; Ig_like.

R InterPro; IPR003006; Ig_MHC.

R PREM; PR0047; IgG.1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS00290; IG_MHC; 1.

T NON_TER 91 91

Q SEQÜENCE 91 AA; 10354 MW; 2F48SA66B6532A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.8%; Score 87; DB 7; Length 91; 100.0%; Pred. No. 3.9e-83; cive 0; Mismatches 0; Indels
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Last annotation update)
   (TremBlrel. 13, Created)
(TremBlrel. 13, Last sequence update)
(TremBlrel. 25, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequent-OCT-2003 (TrEMBLrel. 25, Last annow HLA-C protein (Fragment).
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01-MAY 2000 (TrEMBLrel. 13, Cr 01-MAY 2000 (TrEMBLrel. 13, La 01-OCT-2003 (TrEMBLrel. 25, La MHC class I antigen (Fragment) GGGO-F.
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87; Conservative
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Cianetti L., Testa U., Scotto L., La Valle R., Simeone A., Boccoli G., Giannella G., Peschle C., Boncinelli E.;

"Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of processing.";

Immunogenetics 22:80-21(1989).

-!-FUNCINI INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

-!- FUNCINI INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE MICROGLOBULIN) (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-BMEL) MC4096; AAA59654.1; -...

REMBL; M24096; AAA59654.1; -...

RR GO; GO:0016021; C:integral to membrane; IEA.

RR GO; GO:0016021; C:integral to membrane; IEA.

R INTERFYO: IPRO01309; Ig cl.

R InterPro: IPR001309; Ig cl.

R InterPro: IPR001309; MHC_I.

R InterPro: IPR001309; MHC_I.
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"The classical and non-classical MHC class I genes of pig-tailed

"The classical and non-classical MHC class I genes of pig-tailed

"The classical and non-classical MHC class I genes of pig-tailed

"The classical classical mestrinal.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

BENDI, AY204730; AA084319.1;

REMBL; AY204730; AA084319.1;

RO, GO:00016202; C:membranate; IEA.

RO, GO:00016202; C:membranate; IEA.

RO, GO:0001625; P:immune response; IEA.

RO, GO:00016357; Ig. 1.

RICETPRO; IPR001039; MHC_1.

RICETPRO; IPR001039; MHC_1.

REPAM: PF00129; MHCCLASSI.

REPROPORT: PRO1029; MHCCLASSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 SDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGEE 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.5%; Score 73; DB 7; Length 316; Best Local Similarity 100.0%; Pred. No. 6.5e-68; Matches 73; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00129; MHC I; 1.
Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
PRINTS; PR01638; MHC I; 1.
SMART; SM00407; IGCI; 1.
PROSTTE; PS50835; IG LIKE; 1.
PROSTTE; PS00290; IG MHC; 1.
ACQUICOFOLCIN; Transmembrane.
NON TER 1.
SEQÜENCE 316 AA; 35380 MM; C03B1EC87F75C9BA CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
MMC class I antigen (Fragment).
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RA SEQUENCE FROM N.A.

RA DILINE=20260999; PubMed=10803844;

RA Urater J.A., McAdam S.N., Locharke J.H., Allen T.M., Moran J.L.,

RA Urater J.A., McAdam S.N., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RA Novall T.J., Rojo S., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RT Major histocompatibility complex class I molecules associated with

RT Major histocompatibility complex class I molecules associated with

RT Tesistance and susceptibility, and their relationship to HLA-B27.";

RI Immunogenetics 51:314-325(2000)

C. I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

IMMUNE SYSTEM (BY SIMILARITY).

C. ISUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN) (BY SIMILARITY).

C. SUBUNIT: DROGUESSI (BY MIC. 1: -

DR PROMOTOS) (MC. 1: -

DR PROSITE: PSO0030; MC. 1: -

DR PROSITE: PSO0030; MC. 1: -

DR PROSITE: PSO0300; M
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                             Query Match 22.6%; Score 62; DB 7; Length 314; Best Local Similarity 100.0%; Pred. No. 2.4e-56; Matches 62; Conservative 0; Mismatches 0; Indels
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SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS0290; IG MHC; 1.
NON TER 1 1 1 1 1 SW0VTER 314 AA; 35463 MW; C585496BA90BDC85 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I heavy chain antigen (Fragment).
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Query Match
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RN SEQUENCE FROW N.A.

RA MILLINE-20260999; PubMed=10803844;

RA WEDLINE-20260999; PubMed=10803844;

RA WEDLINE-20260999; PubMed=10803844;

RA TOTALET J.A., McAdam S.M., Loberke J.H., Allen T.M., Moran J.L.,

RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RA Rowell T.J., Rojo S., Lopez de Castro J.B., Taurog J.D., Watkins D.I.;

RA Rowell T.J., Rojo S., Lopez de Castro J.B., Taurog J.D., Watkins D.I.;

RA Rowell T.J., Rojo S., Lopez de Castro J.B., Watkins D.I.;

RA Rominogenetics 5.1.314-325(2000).

RA RADORICO INVOLVED IN THE PRESENTATION OF FOREIGN ANTICENS TO THE CONTROL INVOLVED IN THE PRESENTATION OF FOREIGN ANTICENS TO THE CONTROL OF SIMILARITY).

RANGROGIOBULIN) (BY SIMILARITY).

C. HOMIND SYSTEM (BY SIMILARITY).

C. HOMIN SYSTEM (BY SIMILARITY).

C. HOMIN SYSTEM (BY SIMILARITY).

C. HOROGOSS; LA9F.

C. HOROGOSS; LA9F.

C. GO:0016021; C.integral to membrane; IEA.

BR HOROFT: PRO0129; MHC I; I.

BR PRODOR; PRO0129; MHC I; I.

BR PRODOR; PRO0129; MHC I; I.

BR PROSITE; PSS0835; IG LIKE; I.
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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100.0%; Pred. No. 3e-55;
ive 0; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Created)
10-0CT-2000 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I heavy chain antigen.
                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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OCT-2000 (TREMBLrel. 15, Last sequence up
OCT-2003 (TrEMBLrel. 25, Last annotation
class I heavy chain antigen (Fragment).
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MHC class I }
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Q9MXS5
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                                                                                                         Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0006955; P:immune response; IEA. InterPro; IPR007101; Ig-like. InterPro; IPR003597; Ig c1. InterPro; IPR003006; Ig MHC. InterPro; IPR001039; MHC.
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PROSITE; PS00290; IG_MHC; 1.
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HSSP; P30685; 1A9E.
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Pfam; PF00129; MHC I; 1.
PRINTS; PR010589; MHC LIS:
PEDDOM: PD000050; MHC LIS:
SMART; SM00407; IGC1; 1.
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SEQUENCE 365 AA; 40772 M
                                                 Cercopithecinae; Macaca
NCBI TaxID=9544;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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June 18, 2004, 19:26:37 ; Search time 17 Seconds (without alignments) 839.248 Million cell updates/sec Run on:

US-09-819-371-5 274 1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

141681 segs, 52070155 residues Searched:

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Word size :

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	511 homo	5 pan t	17 macac	3 homo	ошоч Е	09 pan t	39 homo	pan t	pan t	homo	homo	pomor.	homo	homod	рошо			homod	homod	homo	homo		homo	9960 homo	, homo	ропо	pong ?	17693	0383 gor:	13750 pan	16210 pan	P30379 gorilla gor	30380 gor:
SUMMARIES		ID	HLAF HUMAN	1C28 PANTR	HLAF MACMU	HLAH HUMAN	1A01 HUMAN	1A01 PANTR	1A03 HUMAN	1A03 PANTR	1A04_PANTR	1	1A23 HUMAN		1A30 HUMAN	1A36 HUMAN	1C02 HUMAN	1C03 HUMAN	1C04 HUMAN	1C05_HUMAN	1CO6_HUMAN	1C08 HUMAN	1C12 HUMAN	1C14 HUMAN	1C1S HUMAN	1C16 HUMAN		HLAE HUMAN	HLAE PONPY	HLAG HUMAN	1C01 GORGO	1B01 PANTR	1 1	1 1	1B02_GORGO
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P13751 pan troglod P30181 gorilla gor P01889 homo sapien P30460 homo sapien P30464 homo sapien P30464 homo sapien P30466 homo sapien P03989 homo sapien P18463 homo sapien P30475 homo sapien P30475 homo sapien
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                                                                                                                                                                                                                                                                                     1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                        GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                  Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.
EXTRACELIULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                              .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88319000; PubMed=3412487;
Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
"HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.";
Nature 335:268-271(1988).
                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                          100.0%; Score 274; DB 1; Length 362; 100.0%; Pred. No. 1.8e-279; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90201944; PubMed=1690682; Lawlor D.A., Warzen E., Ward F.E., Parham P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-185(1990).
                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
N-LINED (GIGNAC. . .) (BY
V, BRDD041F820A34E1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Pfam; PPO0047; 18; 1.
Pfam; PPO0047; 18; 1.
PRINTS; PR01638; MHCCIASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL.
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TRANSMEM
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CARBOHYD
SEQUENCE
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to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CH28 ALPHA CHAIN.
CR78ACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain F precursor (HLA
                       immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Nacaca.
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FUNCTION: Involved in the presentation of foreign antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 346;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (B)
F03E882D5C2E0971 CRC64;
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Pred. No. 3.4e-124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
HIA Class I histocompatibility antigen, alpha HIA-P OR HIAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
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                                                                                                                                                                                                                                                                              EMBL; M30685; AAA87973.1; -. HSSP; Q30201, 1A6Z.
HXSP; Q30201, 1A6Z.
INTERPRO; IPRO07110; 1G-1ike.
INTERPRO; IPRO03597; IG-1ike.
INTERPRO; IPRO0306; IG MHC.
INTERPRO; IPRO01039; MHC. I.
Pfam; PRO1047; ig; I.
Pram; PRO1047; ig; I.
PRINTS; PRO1058; MHC. I; I.
PRODOM; PRO1058; MHC. I; I.
SNART; SN00407; IGC. I; I.
SNART; SN00407; IGC. I; I.
PROSITE; PSC0835; IG LIKE; I.
MHC I; Transmembrane; Glycoptote
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Best Local Similarity 100.
Matches 126; Conservative
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346 AA;
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                                                                microglobulin)
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P33617;
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TRANSMEM
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HLAF MACMU
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                     MEDLINE=82151002; PubMed=6451010;
Malissen M., Malissen B., Jordan B.R.;
"Exon/intron organization and complete nucleotide sequence of an HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
N-TINKED (GLCNAC. . .) (BY SIMILARITY).
                                                                                             Proc. Natl. Acad. Sci. U.S.A. 79:893-897 (1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A01 HUMAN STANDARD; PRT; 365 AA.
P30443; O77964; O78171; Q9MYA3; Q9TP25; Q9TQP5;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11AA class I histocompatibility antigen, A-1 alpha chain precursor HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%; Score 44; DB 1; Length 362; 100.0%; Pred. No. 3.9e-38; Live 0; Mismatches 0; Indels
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BY SIMILARITY.
OBCDAE8D61A81B86 CRC64;
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HSSP; P03989; 1HSA.
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Matches 44; Conservative
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                        235 BITLTWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPQPL 293
Gaps
                                                                                                                                                     immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, alpha chain H precursor
HLA-AR) (HLA-12.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL) 77BD7E3B9B11E0F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.5%; Score 59; DB 1; Length 348; 100.0%; Pred. No. 6.8e-54; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
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BY SIMILARITY.
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39300 MW;
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nes 59; Conservative
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282
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348 AA;
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P01893;
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DOMAIN
TRANSMEM
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DISULFID
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GN HIA-AI

GN HOMEN

CO EUKARY

CO MARMMALI

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Gaps

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Matches

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Zwan A.W., Bakema J.E., Rozemuller E.H., van der Tweel J.G.,
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      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rusbling Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A litschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A hitschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Batcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Batcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Braplecon M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabs B.M.,
Richards S., Worley W.C., Geren E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rutterfield Y.S.N., Krzywinski M.I., Salaka U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Rederstrion and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                              SEQUENCE FROM N.A. (A*0101).
MEDLINE=88234547; PubMed=3375250;
Parham P., Lomen C.E., Lawlor D.A., Ways J.P., Holmes N., Coppin H.L.,
Salter R.D., Wan A.M., Ennis P.D.;
"Nature of polymorphism in HIA-A, -B, and -C molecules.";
Proc. Natl. Acad. Sci. U.S.A. 85:4005-4009(1988).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*0101).
MEDLINE=98007773; PubMed=9349617;
Laforet M., Froelich N., Parissiadis A., Pfeiffer B., Schell A.,
Faller B., Woehl-Jaegle M.L., Cazenave J.P., Tongio M.M.;
"A nucleotide insertion in exon 4 is responsible for the absence of expression of an HLA-A*01 allele.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95282145; PubMed=7761977;
Browning M.J., Madrigal J.A., Krausa P., Kowalski H.,
Allsopp C.E., Little A.-M., Turner S., Adams E.J., Arnett K.L.,
Bodmer W.F., Parkam P.,
"The HLA-A,B.C genotype of the class I negative cell line Daudi
reveals novel HLA-A and -B alleles.";
Tissue Antigens 45:177-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-206 FROM N.A. (A*0103).
MEDLINE=98101100; PubMed=9438203;
Sitha S., Scheltinga S.A., Johnston-Dow L.A., White C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waller M.J., Robinson J., Marsh S.G.E.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          Warren E.;
Submitted (APR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               SEQUENCE FROM N.A. (A*0101).

MEDLINE=8923515; PubMed=2715640;

Pariam P., Lawlor D.A., Lowen C.E., Ennis P.D.;

Pairam P., Lawlor D.A., Lowen C.E., Ennis P.D.;

Thiversity and diversification of HLA-A,B,C alleles.";

J. Immunol, 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                           Girdlestone J.; "Nucleotide sequence of an HLA-Al gene."; Nucleic Acids Res. 18:6701-6701(1990).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (A*0101).
MEDLINE=91067475; PubMed=2251137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ssue Antigens 50:347-350(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (A*0101).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*0101).
TISSUE=Brain;
                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*0101).
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    NCBI_TaxID=9606;
                                                                                                                                                                                                                                       Warren
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der van Zwan A.W., Bakema J.B., Rozemuller B.H., van der Tweel J.G.,
Kronink M.N., Tilanus M.G.J.;
"A generic sequencing based typing approach for the identification of
HIA-A diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PUTH: SUlfated.
-!- POLYMORPHISM: The following alleles of A-1 are known: A*0101,
A*0102, A*0103, A*0106 and A*0107. The sequence shown is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sant A.J., Zacheis M., Rumbarger T., Giacoletto K.S., Schwartz B.D., "Human Ia alpha- and beta-chains are sulfated.", J. Immunol. 140:155-160(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          я,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-206 FROM N.A. (A*0106).
MEDLINE=20309230; PubMed=10852390;
Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester Ng J., Hartzman R.J., Hurlay C.K.;
"Seventeen more novel HiA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGUENCE OF 26-206 FROM N.A. (A*0107).
Tamouza R., Fortier C., Mahfoudh N., Schaeffer V., Poirier J.C., Marzais F., Gautreau C., Charron D.;
Marzais F., Gautlell.",
"A new HiA-A*01 allell.",
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          SEQUENCE OF 26-206 FROM N.A. (A*0103).

TISSUE=Blood;
MEDLINE=21100775; PubMed=11182232;
Poland G.A., Sohni Y., Domanico M., Kroning C.M., DeGoey S.R., Jimale M., Jacobson R.M., Moore S.B.;
"High frequency of HLA-A*0103 allele in a Somali population.";
Hum. Immunol. 62:197-200(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF214112, AAF19525.1, -.
EMBL, AF214111, AAF19525.1, JOINED.
EMBL, AF142321, AAD33894.1, -.
EMBL, AF142231, AAD33894.1, JOINED.
EMBL, AF219633, AAF73862.1, JOINED.
EMBL, AF219632, AAF73862.1, JOINED.
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MEDLINE=88088800; Pubmed=3121736;
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EMBL; X55710; CAA39243.1; --
EMBL; Z93949; CAB07989.1; --
EMBL; AJZ78305; CAB93537.1; --
EMBL; BC003069; AAH03069.1; --
EMBL; Y12469; CAA73072.1; --
EMBL; Y12470; CAA73073.1; --
                                                                                                                Hum. Immunol. 57:120-128(1997).
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PIR, 161856; 161856.
HSSP; 019673; 1HSB.
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us-09-819-371-5.0li.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
(FC452786BD038D3E CRC64;
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1D 1A03 HUMAN STANDARD; PRT; 365 AA.

C P0439; O19546; O19756; Q9GJE6; Q9GJE7; Q9GJE8; Q9MYG4; Q9TPR8;

DT 13-AUG-1987 (Rel. 05, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE HLA class I histocompatibility antigen, A-3 alpha chain precursor

DE MHC class I antigen A*3).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-84207948; PubMed-6609814; Strachan B.R.; Strachan T., Sodoyer R., Damotte M., Jordan B.R.; M.Complete nucleotide sequence of a functional class I HLA gene, HLA-A3: implications for the evolution of HLA genes."; BMBO J. 3:887-894(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30679; AAA89970.1; --
PIR; I36961; I36961.
HSSP; Q95352; IHTM.
INTERPRO; IPR001319; IG-11; INTERPRO; IPR001359; IG-21.
INTERPRO; IPR001399; MHC.
INTERPRO; IPR001039; MHC.
INTERPRO; IPR001039; MHC.
Pfam; PP00129; MHC. I:
PFAM; PR00129; MHC. I:
PRNTYE; PR01688; MHCCLASSI.
PRODOM; PD000050; MHCI.
PROSITE; PS00290; IG-MHC; I.
PROSITE; PS00290; IG-MHC; I.
MHC I; Transmembrane; Glycoptote
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Ellexson M.E., Hildebrand W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40848 MW;
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365 AA;
                                               microglobulin).
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SEQUENCE
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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01-APR-1990 (Rel. 14, Last seguence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, A-2 alpha chain precursor.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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/FIG=VAR 004332.

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G-> R (in aliele A*0102).
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44; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santos S., Balas A., García-Sanchez F., Lillo R., Merino J.L., Vicario J.L., "Complete cDNA coding sequence of a new HLA-A3 subtype (A*0304) with a new HLA polymorphism at exon 3."; Immunogenetics 49:360-361(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
POLYMORPHISM: The following alleles of A-3 are known: A*0301
(A-3.1), A*0302, A*0304 and A*0305. The sequence shown is that of A*0301.
                                                                                                            HLA class I region.";
                                                                                                                                                SEQUENCE FROM N.A. (A*0302).
MEDLINE-85290817;
MEDLINE-85290817; PubMed-2593417;
Molecular cloning and DNA sequence analysis of genes encoding cytotoxic T lymphocyte-defined HLA-A3 subtypes: the E1 subtype.";

[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poli F., Frison S., Crespiatico L., Longhi E.;
"Identification of a HLA-A*03 new variant.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in the presentation of foreign antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE OF 26-206 FROM N.A. (A*0305).
Becher M.P., Wu J., Williams T.,
"Novel human HLA-A alleles identified in potential bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the immune system.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*0302).
Bettinotti M.P., Hadzikadic L., Adams S., Marincola F.M.;
"Complete coding sequence of HLA-A*0302.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                      SEQUENCE FROM N.A. (A*0301).
Shiira S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 5p21.3 HiA clas
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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GO: GO: GO: C:integral to plasma membrane; NAS.
GO: GO: GO: 0010106; F:MHC class I receptor activity; NAS.
GO: GO: 0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-298 FROM N.A. (A*0305).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X00492; CAA25162.1; ALT_SEQ.
EMBL, U32184; AAB63980.1;
EMBL, AP000520; BAB63400.1;
EMBL, AF010519; BAB63400.1; JOINED.
EMBL, AF015930; AAB6682.1;
EMBL, AF19719; AAF63243.1;
EMBL, AF190719; AAF63243.1;
EMBL, AF190718; AAF60368.1;
EMBL, AJ401086; CAC06088.1;
EMBL, AJ401086; CAC06088.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (A*0304).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-341 FROM N.A. (A*03)
MEDLINE=99180630; PubMed=10079303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:4931; HLA-A.
MIM; 142800; -.
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HSSP; O19673; 1HSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissum=Blood;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-ARF-1993 (Rel. 25, Last sequence update)
01-ARF-1993 (Rel. 25, Last sequence update)
CHLA class I histocompatibility antigen, A-108 alpha chain precursor.
Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
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DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MEC.

DR InterPro; IPR003006; Ig_MEC.

DR InterPro; IPR001039; MHC_I.

DR Pfau; PF00047; ig; 1.

R Pfau; PF00047; ig; 1.

R ProDom; PD000050; MHC_I; 1.

R ProDom; PD000050; MHC_I: 1.

R SWART; SM00407; IGC1; 1.

R PROSITE; PS00290; IG_MHC_I; 1.

R PROSITE; PS00290; IG_MHC_I: 1.

R PROSITE; PS00290; IG_MHC; 1.

R PROSITE; PS00290; IG_MHC; 1.

R PROSITE; PS00290; IG_MHC; 1.

R PROSITE; PS00290; IG_MHC; 1.
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Mayer W.E., Jonker M., Klein D.; Ivanyi P., van Seventer G.
Klein J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1%; Score 44; DB 1; Length 365; 100.0%; Pred. No. 3.9e-38; tive 0; Mismatches 0; Indels
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BY SIMILARITY.

E - V (in allele A*0302).

FTId=VAR 004351.

L - Q (in allele A*0302).

FTId=VAR 004352.

D - E (in allele A*0305).

FTId=VAR 016604.

G -> R (in allele A*0304).

FTIG=VAR 016605.

FTIG=VAR 016605.

W, DEDFCEC4450E0580 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 QIQDIELVETRPAGDGTPQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 OTODTELVETRPAGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                     A-3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
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or send an email to license@isb-sib.ch)
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TRANSMEM
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBO J. 7:2765-2774(1988).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
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P13749;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, A-126 alpha chain precursor.
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-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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MEDLINE-89030641; PubMed=2460344;
Mayer W.B., Jonker M., Klein D., Ivanyi P., van Seventer G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 365;
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (B)

48CC757055221FC3 CRC64;
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
24
                                                                                EMBL; X13113; CAA31505.1; ALT_INIT.
PIR; S03535; S03535.
                                                                                                                    HSSP, O19673, IHSB.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG-like.
InterPro; IPR001039; MHC_I.
Pfam; PP00047; ig; I
Pfam; PP00129; MHC_I.
Pfam; PP00129; MHC_I.
ProDom; P00129; MHC_I.
ProDom; P001096; MHC_I.
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SEQUENCE
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Nucleotide seguences of chimpanzee MHC class I alleles: evidence for
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HLA-All split antigens, All.1 and
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P13746; 019605; 019606; 029747; 029835; 09BCN0; 09MXI5; 09TQE9; 0197026; 09TQP1
01-7074-1990 (Rel. 13, Created)
01-7074-1990 (Rel. 13, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
HIA class I histocompatibility antigen, A-11 alpha chain precursor HIA-A OR HLAA.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Klein J.;
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MEDLINE=94287401; PubMed=8016845;
Lin L., Tokunaga K., Ishikawa Y., Bannai M., Kashiwase K.,
Kuwata S., Akaza T., Tadokoro K., Shibata Y., Ouji T.;
"Sequence analysis of serological HLA-All split antigens, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 16.1%; Score 44; DB 1; Length 365; Similarity 100.0%; Pred. No. 3.9e-38; 44; Conservative 0; Mismatches 0; Indels
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D3C9A810B22A768F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 QIQDIELVETRPAGDGTFQKWAAVVVPSGEEQRYICHVQHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTODTELVETRPAGDGTFOKWAAVVVPSGEBORYTCHVOHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-126 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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BY SIMILARITY.
BY SIMILARITY.
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MEDLINE-89030641; PubMed=2460344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-365 FROM N.A. (A*1101).
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EMBO J. 7:2765-2774(1988).
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
Pfam; PF00129, MHC 1; 1.
Prints; PR01629; MHCCLASSI.
ProDom; PD000050; MHC 1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotisional control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                                                  HSSP, 019673, IHSB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597, Ig_cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR001039, MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40656 MW;
EMBL; X13114; CAA31506.1;
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                                                       PIR; S01171; S01171
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the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0005897; C: integral to plasma membrane; NAS.
R GO; GO: 000106; F:MHC class I receptor activity; NAS.
R GO; GO: 000106; F:MHC class I receptor activity; NAS.
R GO; GO: 00055; P: immune response; NAS.
R InterPro; IPR003597; Ig_cl.
R InterPro; IPR003597; Ig_cl.
R InterPro; IPR001039; MHC.
R InterPro; IPR001039; MHC.
R Pfam; PF00047; Ig; 1.
R PRINTS; PR001039; MHC.I; 1.
R PRINTS; PR000050; MHCLIS: 1.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS00290; IG_MIC. 1.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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N-LINKED (GLCNAC. . .) (BY SIN BY SIMILARITY.

BY SIMILARITY.

S -> SGGEGVK (in isoform 2).

FTIGAVAR 008099.

F -> L (in allele A*1102).

FTIGAVAR 016731.

K -> E (in allele A*1105).

FTIGAVAR 016731.

K -> E (in allele A*1105).

FTIGAVAR 016731.

K -> E (in allele A*1103).

FTIGAVAR 016732.

FTIGAVAR 016733.

FTIGAVAR 016733.

FTIGAVAR 016733.

FTIGAVAR 016733.

FTIGAVAR 016733.

FTIGAVAR 016733.

FTIGAVAR 016734.

FTIGAVAR 016734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF030910; AAB87052.1; EMBL; AF030909; AAB87052.1; EMBL; AF030909; AAB87052.1; EMBL; AF030909; AAB87052.1; EMBL; AF030909; AAB87051.1; OINED. EMBL; AJ306733; CAC37336.1; EMBL; AF147455; AAD33991.1; OINED. EMBL; AF147454; AAD33991.1; OINED. EMBL; AF165065; AAF25781.1; OINED. EMBL; AR165065; AAF25781.1; OINED. EMBL; AR165065; AAF25781.1; OINED. EMBL; AR165065; AAF25781.1; OINED. EMBL; AR16506; AAF25781.1; OINED. EMBL; AR16506; AAF25781.1; OINED. EMBL; AAF366; AAF
                                                                                                                                                  EMBL, X13111, CAA31503.1, EMBL, X13112, CAA31504.1, EMBL, D16841, BAA04117.1, EMBL, D16842, BAA04118.1, EMBL, M16010, AAA65449.1, TOINED EMBL, M16009, AAA65449.1, JOINED EMBL, M16009, AAA65449.1, JOINED EMBL, Y17224, CAB38056.1, EMBL, X17224, CAB38056.1, EMBL, X91399, CAA62745.1,
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
EMBL;
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissen H.J., Sisternans E.A., Joosten I.;
"A unique second donor splice site in the intron 5 sequence of the HLAA-*11 alleles results in a class I transcript encoding a molecule with an elongated cytoplasmic domain.";
Tissue Antigens 55:422-428(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-206 FROM N.A. (A*1105).
MEDLINE=20309230; PubMed=10852390;
Blis J., Steiner N.K., Koeman C., Henson V., Mitton W., Koester R., Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HHA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           population.";
Tissue Autigens 58:190-192(2001).
-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonyms=Long;
Isold=P13746-2; Sequence=VSP_008099;
Note=Cnly produced by allele A*1103;
POLYMORPHISM: The following alleles of A-11 are known: A*1101
(A-11E), A*1102 (A-11K), A*1103, A*1104, A*1105 and A*1107. The sequence shown is that of A*1101.
                                                                                                                                                                                                                                              Tijssen H.J., Sistermans E.A., van den Beucken M.J.G., Krausa P., Joosten I.;
  MEDLINE=87192928; PubMed=2437024; Cowan E.P., Jelachich M.L., Biddison W.E., Coligan J.E.; Cowan E.P., Jelachich M.L., Eddison W.E., Coligan J.E.; "DNA sequence of HiA-All: remarkable homology with HiA-Al allows anchitication residues involved in epitopes recognized by antibodies and T cells."; "Immunogenetics 25:241-250(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (A*1105).
MEDLINE=99321035; PubMed=10395112;
Mortell G., Whalley J., Stewart A., Day S., Lewis L., Makar Y.,
Ross J., Dunn P.P.;
"Identification of an HIA-All serological variant and its
characterization by sequencing based typing.";
Tissue Antigens 53:591-594(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-206 FROM N.A. (A*1104).
Chandanayingyong D., Sirikong M., Luangtrakool K., Srinak
Rungroung E., Belohandra S.;
"All alleles (A*1104) ",
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bettinotti M.P.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the A*1103 allele."; Tissue Antigens 55:68-70(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing, Named isoforms=2,
Name=1,
IsoId=P13746-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2) (A*1103).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (A*1107).
MEDINES-1561663; PubMed=11703829;
Pyo C.W., Choi H.B., Han H., Hong Y.S.
"Identification of HLA-A*11 variant (A
                                                                                                                                                                                   SEQUENCE FROM N.A. (A*1103).
TISSUE=Blood;
MEDLINE=20166353; PubMed=10703613;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20340071; PubMed=10885562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (A*1104).
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Blood
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SEQUENCE FROM N.A. (A*2301).
MEDLINE=92104637; PubMed=1729171;
Little A.-M., Madrigal J.A., Parham P.;
Little A.-M., Madrigal J.A., Parham P.;
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Seven novel HLA-A alleles carry previously observed polymorphisms.";
Tissue Antigens 56:551-552(2000).
-!- FUNCTION: Involved in the presentation of foreign antigens to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- POLYMORPHISM: The following alleles of A-23 are known: A*2301, A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of A*2301.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1A23 HUMAN STANDARD; PRT; 365 AA.
1A23 HUMAN STANDARD; Q9TQGS; Q9TQGS; Q9TQRI;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester
Ng J., Hartzman R.J., Huxley C.K.;
"Seventeen more novel HiA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
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Hurley C.K.,
                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                   224 OTODIELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 ÓTÓDTELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 291
                                                                                                                                                                                                                                                                                                         0; Indels
     T -> S (in allele A*1105).
                                                          /FTId=VAR_016736.
40937 MW; FE449CEZD4BF6CC5 CRC64;
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MEDLINE=21068830; PubMed=11169246;
                                                                                                                                                                                               uery Match
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
fatches 44; Conservative 0; Mismatchés 0;
                                                     /FTIG=VAR
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                                                                                                               365 AA;
          345
                                                                                                               SEQUENCE
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          VARIANT
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P05534; P30448; P30449; Q29908; Q29910; Q95355;
P05534; P30488 (Rel. 09, Created)
10-007-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
(MHC class I histocompatibility antigen, A-24 alpha chain precursor HLA-A OR HLAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                  DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR001399; Ig_cl.
DR InterPro; IPR001039; MHC_l.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_l. 1.
DR PRINTS; PR01638; MHC_L! 1.
DR PRINTS; PR01638; MHC_L! 1.
DR PRNAT; SN00050; MHC_l: 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC_l.
DR PROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y -> C (in allele A*2305).

/FTId='VAR 016606.

K -> N (in allele A*2303).

/FTId='VAR 016607.

L -> W (in allele A*2302).

/FTId='VAR 016608.

DG -> EW (in allele A*2304).

/FTId='VAR 016609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
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C372DE503BF393D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A-23 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Pred. No. 3.9e-38;
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100.0%; Pred. No. ...
... 0; Mismatches
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SEQUENCE FROM N.A. (A*2402 AND A*2403).
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MEDLINE=85206128; PubMed=2987115;
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HGNC:4931; HLA-A.
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1A24 HUMAN
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CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                          CLASS I HISTOCOMPATIBILITY ANTIGEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 OTODIELVETRPACDGIFOKMAAVVVPSGEEQRYICHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 QIQDIELVETRPAGDGIFQKWAAVVVPSGEEQRYICHVQHEGLP 291
                                                                                                                                                                                                                                                            Glycoprotein; Signal; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 206 T -> A (in allele A*2401).
/PTId=VAR 004360.
365 AA; 40688 MW; D33684D126F98EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTIG=VAR_004358.
I -> R (in allele A*2410).
FTIG=VAR_015770.
                                                                                                                                                                                                                                                                                                                      EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR 004359
                                                                                                                                                                                                                                                                                                            A-24 ALPHA CHAIN
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EMBL; U18987; AABG0651.1; JOINED.
PIR; I54416; I54416.
MSSP; Q95352; 1HHK.
Genew; HGNC:4931; HLA-A.
MIM; 142800;
                                                                         MIME, 142200; ---
INTERPRO; IPRO07110; IG-like.
INTERPRO; IPR003597; IG_C1.
INTERPRO; IPR003065; IG_MGC.
INTERPRO; IPR001039; MHC_I.
Pfam; PF00129; MHC_I; 1.
Pfam; PF00129; MHC_I; 1.
Pfam; PF00129; MHC_I; 1.
PRONSITE; PS06085; IG_LIKE; 1.
PROSITE; PS060835; IG_LIKE; 1.
PROSITE; PS060835; IG_LIKE; 1.
PROSITE; PS06290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotes
                                                                                                                                                                                                                                                                                                                                          206
208
3332
283
283
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DISULFID
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1D 1A30_HT
AC P16188;
DT 01-APR-
DT 01-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Blood,

MEDLINE-9741771; PubMed-9271829;

MEDLINE-97417771; PubMed-9271829;

TISSUE-Blood,

Three newly identified A*24 Bileles: A*2406, A*2413 and A*2414.";

Three newly identified A*24 Bileles: A*2406, A*2413 and A*2414.";

Trissue Antigens 50:192-196(1997).

I Tissue Antigens 50:192-196(1997).

-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- POLYMORPHISM: The following alleles of A-24 are known: A*2401, A*2402.

-!- POLYMORPHISM: The following alleles of A-24 are known: A*2401, A*2402.

A*2402, A*2403, A*2408, A*2408, Allele A*2413 are found in the Australian Aborigenal population. Allele A*2413 are found in individuals of South American descent. The sequence shown is that
                      P.;
third HLA-A9 molecule: HLA-A9.3.";
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SEQUENCE FROM N.A. (A*2402).
SEQUENCE FROM N.A. PubMed=9349616;
Laforet M., Froelich N., Parissiadis A., Bausinger H., Pfeiffer B.,
Tongio M.M.;
Tongio M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97161044; PubMed=9008316;
Gao X., Matheson B.;
"A novel HLA-A*24 (A**410) identified in a Javanese population.";
Tissue Antigens 48:711-713(1996).
                                                                                                   MEDLINE=92269955; PubMed=1317015; Mellich P., Madrigal U.A., Hildebrand W.H., Zemmour J., Williams R.C., Luz R., Petzl-er M.L., Parham P.; "Unusual HIA-B alleles in two tribes of Brazilian Indians.";
                                                                                                                                                                                                                                                                                                                                                        Kashiwase K., Tokunaga K., Ishikawa Y., Qiu L., Furuya M., Sawanaka K., Akaza T., Tadokoro K., Juji T.;
"A new A9 sequence HLA-A9HH from Japanese.";
MHC 3:9-14(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 26-206 FROM N.A. (A*2406; A*2413 AND A*2414),
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-206 FROM N.A. (A*2410)
     MEDLINE-92104637; PubMed=1729171;
Littla A. M. Madrigal U.A., Parham
"Molecular definition of an elusive
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M15497; AAA59611.1; ...
EMBL; M64741; AAA59600.1; ...
EMBL; M64741; AAA59600.1; ...
EMBL; Z72422; CAA96532.1; ...
EMBL; D83516; BAA11936.1; ...
EMBL; U37111, AAA83264.1; JOINED.
EMBL; U37110; AAA83265.1; ...
                                                                                                                                                                                                                                                                                                 Lissue Antigens 50:340-346(1997)
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (A*2408).
                                                                                       SEQUENCE FROM N.A. (A*2402)
                                                                                                                                                                    Nature 357:326-329(1992).
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rissum=Blood;

TISSUE=Blood

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Gaps

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0; Indels

1730 HUMAN STANDARD; PRT; 365 AA. 17430 HUMAN STANDARD; P30452; Q9UIP7; 01-APR-1990 (Rel. 14, Created) (Rel. 14, Created) 1-FBB-1996 (Rel. 33, Last sequence update)

AAA83265.1; JOINED. AAB40048.1; -. AAB40048.1; JOINED.

U37112; 7 U37115; 7 U37114; 7 U19733; 7

EMBL; EMBL; EMBL; EMBL;

AAB60651.1;

Length 365;

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MEDILINE=96058597; PubMed=6522453; Krausa P., Carcassi C., Orru S., Bodmer J.G., Browning M.J., Contu L.; Krausa P., Carcassi C., Orru S., Bodmer J.G., Browning M.J., Contu L.; "Defining the allelic variants of HLA-A30 in the Sardinian population using applification refractory mutation system -- polymerase chain reaction.";
                                                                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A. (A*3001).

SEQUENCE FROM N.A. (A*3001).

MEDLINE=90038496; PubMed=2476623;

Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;

Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;

MOLECULar analysis of the secologically defined HLA-Aw19 antigens. A genetically distinct family of HLA-A antigens comprising A29, A31, A32, and Aw33, but probably not A30.";

J. Immunol. 143:3371-3378(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olerup O., Daniels T.J., Baxter-Lowe L., "Correct sequence of the A*3001 allele obtained by PCR-SSP typing and automated nucleotide sequencing."; Tissue Antigens 44:265-267(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [6]
SEQUENCE OF 26-206 FROM N.A. (A*3004).
MEDLINE=96435464; PubMed=8838350;
MEDLINE=96435464; PubMed=8838350;
Lienert K., Russ G., Bennett G., Gao X., McCluskey J.;
"HLA-A*3004: a new A30 allele identified in an Australian Caucasoid population:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Diversity is demonstrated in class I HLA-A and HLA-B alleles in cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-B*1403, *4016, *4703."; Tissue Antigens 56:291-302(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 28-205 FROM N.A. (A*3004).
MEDLINE=96124443; PubMed=8560452;
Blasczyk R., Wehling J., Paessler M., Hahn U., Huhn D., Salama A.;
An novel HIA-A30 allele (A*3004) identified by single-strand
-conformation polymorphism analysis and confirmed by solid-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (A*3002).

MEDILINE-93056508; PubMed-1431115;

MEDILINE-93056508; PubMed-1431115;

MATIGAL J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,

Little A.W., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,

Martell R.W., du Toit E.D., Parham P.;

Martell R.W., du Toit E.D., Parham P.;

interallelic conversion.";

J. Immunol. 149:3411-3415(1992).
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, A-30 alpha chain precursor
(MHC class I antigen A*30).
                                                                                                                                                                            Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [4]
SEQUENCE OF 25-279 FROM N.A. (A*3003).
MEDLINE=93209813; PubMed=8458735;
Choo S.Y., Starling G.C., Anasetti C., Hansen J.A.;
Choo S.Y. at an unrelated donor for marrow transplantation
"Selection of an unrelated donor for marrow transplantation
facilitated by the molecular characterization of a novel HLA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-206 FROM N.A. (A*3006).
MEDLINE=20548605; PubMed=11098929;
Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
Hurley Ç.K.;
                                                                                                                                                                            Craniata; Vertebrata; Butele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Antigens 46:322-326(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (A*3001).
MEDLINE=95176329; PubMed=7871528;
                                                                                                                                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum. Immunol. 44:35-42(1995).
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SEQUENCE FROM N.A. (A*3004)
                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                               HLA-A OR HLAA.
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                                                                                                SECURNCE FROM N.A. (A*3008).
MEDLINE=21108617; PubMed=11165261;
Cox S.T., Morthinin A.J., Koester R.P., Heine U., Holman R.,
Madrigal A.J., Little A.M.,
"Further diversity at HLA-A and -B loci identified in Afro-Caribbean potential Dome marrow donors.";
Tissue Antigens 57:70-72(2001).
-!-FUNCTION: Involved in the presentation of foreign antigens to
                                                                                                                                                                                                                  the immune system.
                                고.
                                                                                                                                                                                                                                                           -1- SUBCELLUIAR LOCATION: Type I membrane protein.
-1- POLYMORPHISM The following alleles of A-30 are known: A*3001 (A30.3), A*3002, A*3003, A*3004 (A30W), A*3006, A*3007 and A*3008. The sequence shown is that of A*3001.
                                   V., Mitton W., Koester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MINI, 1420005. ...

R GO; GO:0005887; C:integral to plasma membrane; NAS.

R GO; GO:0005887; C:integral to plasma membrane; NAS.

R GO; GO:000106; F:iMC class I receptor activity; NAS.

GO; GO:0005955; P:immune response; NAS.

R InterPro; IPRO0110; Ig-like.

R InterPro; IPRO03597; Ig C1.

R InterPro; IPRO03006; Ig-MHC.

R InterPro; IPRO03006; Ig-MHC.

R Pfam; PRO047; ig; 1.

R PRINTS; PRO00050; MHC_I: 1.

R PRINTS; PRO00050; MHC_I: 1.

R PROSITE; PS50835; IG LIKE; 1.

R PROSITE; PS50835; IG LIKE; 1.

R PROSITE; PS00290; IG-MHC; 1.

R MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
SEQUENCE OF 26-206 FROM N.A. (A*3007).
MEDLINE=20309230; PubMed=10852390;
Bllis J., Steiner N.K., Kosman C., Henson V.,
Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
Issue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M305'6; AAAS9612 1; EMBL, U07234; AAA70162.1; EMBL, X61702; CAA43871.1; EMBL, M3365'7; AAA58650.1; EMBL, U3734; AAA58650.1; EMBL, U19734; AAB53658.1; EMBL, U19734; AAB53658.1; EMBL, W32424; AAB53658.1; EMBL, X83770; CAA58723.1; EMBL, X83771; CAA58723.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; 138519; 138519.
PIR; 156039; 156039.
HSSP; Q95352; 1HHK.
Genew; HGNC:4931; HLA-A.
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                                                                                  Rizzuto G.A., Hurley C.K.;
"Novel HIA-A Allele";
"Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                     microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of A-36 are known: A*3601 and A*3602. The sequence shown is that of A*3601.
                                                                                                                                             immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
Martell R.W., du Toit B.D., Parham P.; "Distinctive HLA-A,B antigens of black populations formed by interallelic conversion."; Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 OTODIELVETRPAGDGIFOKWAAVVVPSGEEORYICHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> A (in allele A*3602).
/FTId=VAR 016610.
E -> D (in allele A*3602).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTIG=VAR 016611.
40934 MW; BA00A0085989CD3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-36 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1; Le
Pred. No. 3.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; Scor.
100.0%; Pred. No. 5..
'.. 0; Mismatches
                                                                     SEQUENCE OF 26-206 FROM N.A. (A*3602)
                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF274505, AAF78082.1; --
EMBL, AF74504, AAF78082.1; JOINED.
PIR, 133478; 137478.
HSSP, Q95352; 1HHK.
                                                                                                                                                                                                                                                                                                                                                               EMBL; X61700; CAA43869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:4931; HLA-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 44; Conserv
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Matches
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                                                                                                                       N-LINKED (GLCWAC. .) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

H -> Q (in allele A*3002, allele A*3004

and allele A*3008).

Fride-VAR 004366.

S -> Y (in allele A*3008).

Fride-VAR 010284.

T -> A (in allele A*3006).

Fride-VAR 06653.

R -> G (in allele A*3005).

Fride-VAR 064867.

Fride-VAR 064867.

Fride-VAR 064867.

Fride-VAR 064867.

C -> E (in allele A*3007).

Fride-VAR 016738.

RN -> GK (in allele A*3007).

Fride-VAR 016738.

C -> H (in allele A*3007).

Fride-VAR 016738.

O -> H (in allele A*3007).

A*3004, allele A*3004, allele A*3005.
                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG=VAR_004368.
VD -> EN (in allele A*3002, allele
A*3003, allele A*3004, allele A*3006 and
allele A*3007).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W -> R (in allele A*3002, allele A*3003
and allele A*3007).
/FIId=VAR_004371.
               CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A36 HUMAN STANDARD; PRI; 365 AA.
P30455; OPMY89;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
110-CCT-2003 (Instruction update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR 004369.
RW -> HV (in allele A*3004 and allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_004371.
L -> W (in allele A*3004 and allele
A*3006).
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0
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Pred. No. 3.9e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S -> F (IN REF. 1).
521166D95FB1DC28 CRC64;
                           A-30 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VAR 004370.
                                                                                                                 CYTOPLASMIC TAIL.
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100.0%;
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                                           55
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365 AA;
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1115
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2007
3009
333
1110
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227
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TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
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 SIGNAL
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1A36_HUMAN
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Gaps

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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (CW*0202).

MEDLINE=8921515; PubMed=2715640;

Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;

"Diversity and diversification of HLA-A,B,C alleles.";

J. Immunol. 142:3937-3950(1989).

-: FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                           [1] SEQUENCE FROM N.A. (CW*0201).
SEQUENCE FROM N.A. (CW*0201).
MEDLINE=89215297; FubMed=2708822;
Ellis S.A., Strachan T., Palmer M.S., McMichael A.J.;
"Complete nucleotide sequence of a unique HLA class I C locus product
"Complete nucleotide sequence of a unique HLA class I C locus product
expressed on the human choricoarcinoma cell line BeWo.";
J. Immunol. 142:3281-3285(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIA CIASS I HISTOCOMPATIBILITY ANTIGEN, CW-2 ALPHA CHAIN.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                   -i- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                 microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of Cw-2 are known: Cw*0201 (Cw2.1) and Cw*0202 (Cw2.2). The sequence shown is that of Cw*0201.
                                 1CO2 HUMAN STANDARD; PRT; 366 AA.
P30501; P30502;
P30501, P30502;
O1-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, Cw-2 alpha chain precursor (HLA-C OR HLAC.
HUMC class I antigen Cw*2).
HOME ospiens (Human)
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
366
                                                                                                                                                                                                                                                                                                                                         immune system.
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115
207
299
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DOMAIN
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                     CHAIN
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                                                N-INNED GLCMAC. .) (BY SIMILARITY).

E -> A (in allele Cw*0202).

FTIG4-VAR 016556.

/FTIG4-VAR 016557.

GR -> AP (in allele Cw*0202).

/FTIG4-VAR 016557.

/FTIG4-VAR 016557.

/FTIG4-VAR 01658.

N -> K (in allele Cw*0202).

/FTIG4-VAR 01658.

K -> T (in allele Cw*0202).

/FTIG4-VAR 01656.

K -> T (in allele Cw*0202).

/FTIG4-VAR 01656.

                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 366;
Pred. No. 3.9e-38;
                                                                                                                                                                                                                                                                                                                                                                            224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                      248 ÓTÓDTELVETRPAGDGTFOKWAAVVVPSGEEGRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                       FTId=VAR 016562.
AD8025DEB7DA8CE6 CRC64;
            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                 16.1%; Score 44; DB
ilarity 100.0%; Pred. No. 3.9
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                     366 AA; 41095 MW;
333
366
188
110
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3309
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Best Local Simil
Matches 44; (
              DOMAIN
DISULFID
DISULFID
                                                           CARBOHYD
VARIANT
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Search completed: June 18, 2004, 19:30:22 Job time: 17 secs

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MHC class I histochic class I protein MHC class I protein MHC class I protein MHC class I protein MHC class I histochic 
                                                                                                                                                                     June 18, 2004, 19:28:12; Search time 20 Seconds (without alignments) 1317.824 Million cell updates/sec
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274
1 GSHSLRYPSTAVSRPGRGSP......QRYTCHVQHEGLPQPLILRW 274
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283366 seqs, 96191526 residues
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                                                                                                                 OM protein - protein search, using sw model
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C3071184

C3071184

C3071186

C20990

C4499

C56424

C56424

C66424

C
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*
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Match 1
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                     Sequence:
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No.
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ss I hist	MHC class I histoc	MHC class I histoc	MHC class I histoc	class I				MHC class I histoc	HLA-Cw2.	class I	MHC class I histoc	lymphocyte antigen	lymphocyte antigen	MHC class I histoc	MHC class I histoc
JS0262	B37028	S42823	137523	JH0526	137527	172113	138507	137526	161866	I38505	168712	181231	I81232	137544	137135
N	N	~	N	7	0	~	~	~	N	N	N	N	N	N	N
366	366	366	366	366	366	366	366	366	366	366	366	366	366	366	366
16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1
44	4	44	44	44	44	44	44	44	44	44	44	44	44	44	44
30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

ALIGNMENTS

RESULT A60384	and the the Down
MHC CLA.	y antigen h <u>ra-r</u> alpna chain bews precursor -
C, Date:	C.Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Jul-1999 C.Accession: A60384: JL0147
R, Lury,	Rilury, D.; Epstein, H.; Holmes, N.
A;Title	Alitie: The human class I MHC gene HLA-F is expressed in lymphocytes.
A; Rezer A; Acces	A;Kererence number: Abusa4; Muld:9119/889; FM1D:1/0/859 A;Accession: A60384
A; Moleci	A; Molecule type: DNA a:pesidner: 1-362 cIMR>
R, Gerag	R, Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.
J. Exp. A,Title	Med. 171, 1-18, 1990 : Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a cl
A; Refer	
A; Acces A; Molec	sion: JL0147 ule type: DNA
A, Resid	
A; Cross	A;Cross-references: GB:X17093; NID:g32223; PIDN:CAA34947.1; PID:g31240/
C.Genetics:	
A; Gene:	:HLA-F
A, Cross	-references: GDB:125714
A: Intro	OSICION: 0/21:3-0/21:3 n8: 22/1: 112/1: 204/1: 296/1: 335/1: 346/1: 362/1
C, Super	family: class I histocompatibility antigen; immunoglobulin homology
C; Keywo	rds: glycoprotein; heterodimer; transmembrane protein Domain: signal segmence #status predicted <sig></sig>
F; 22-11	1/Domain: alpha-1 <ali></ali>
F;78-10	4/Region: hypervariable
F;112-2 F:164-1	03/Domain: aipna-z <abz> 92/Region: hypervariable</abz>
F;204-2	95/Domain: alpha-3 <al3></al3>
F;217-2 F;107/B	F:ZII-ZBZ/DOMBAIN: Immunoglobulin nomology <pre></pre>
Query	Ouery Match 100.0%; Score 274; DB 2; Length 362;
Best Loc Matches	cal Similarity 100.0%; Pred. No. 3274; Conservative 0; Mismatch
ò	1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTGFLRFDSDAAIPRMEPREPRVEQEGEQYW 60
î	S S S S S S S S S S S S S S S S S S S
aa	
δλ	61 EWTIGYAKANAQTDRVALRNLIRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
qq	82 EWITGYAKANAQIDRYALRNILIRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 141
δ	121 XDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEFRTYLEGGCLELLRRYLENGKETLQ 180

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